

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number:113398

TO: Michael Borin

Location: rem/2a55/2c70

Art Unit: 1631

Wednesday, February 04, 2004

Case Serial Number: 09/582486

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Borin,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

Run on:

February 3, 2004, 17:33:58 ; Search time 21 Seconds (without alignments) 1424.212 Million cell updates/sec

US-09-582-486-1 1637 1 MDTTVPTFSLAELQOGLHQD.....ATFQDWIGGNYVNIRRTSKA 311

litle:
Perfect score:
sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

fotal number of hits satisfying chosen parameters: 283308 segs, 96168682 residues

searched:

283308

finimum DB seq length: 0 faximum DB seq length: 2000000000

maries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 % PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* atabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	deacetoxycephalosp	deacetoxýcephalosp	isopenicillin N sv	sopenicillin N	Z	Z	g	probable gibberell	isopenicillin N sv	probable dioxygena			isopenicillin N sv	qibberellin 20-oxi	flavonol synthase	isopenicillin N sv	probable iron/asco	isopenicillin N sv	gibberellin 20-oxi	gibberellin 20-oxi	iron deficiency ar	isonenicillin N sy							
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SUMMARIES				_	_		_					_	_																	
SU	£	m	A32043	830900	840253	A39204	S54100	A29711	S54101	A61155	A29894	808218	S54099	D84713	D96635	B32344	C84713	833510	S15284	A58458	T48491	T07373	A26467	AG0160	S04441	T11847	T11849	T05903	A27355	T09664
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	Length	311	311	314	310	318	319	332	313	329	329	326	326	362	376	333	358	348	328	321	380	349	331	355	331	382	370	339	331	386
* Query	Match	99.5		72		57.	57.		25.	_	9		9	В.	œ.	œ	8.7	8.6	8.4			8.2		8.0	7.9		7.6	7.5	7.5	7.5
	Score	1629	1627	1186.5	965.5	939.5	937	926.5	852	176	164	162	162	146.5	144.5	143	142.5	140	138	~		134.5	133.5	131.5	129.5	125	124.5	123	122.5	122.5
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probable gibberell	leucoanthocvanidin	leucoanthorvanidin	qibberellin 20-oxi	naringenin 3-dioxv	SRG1 protein - Ara	1-aminocyclopropan	probable exidered	SRG1 protein-relat	gibberellin 20-oxi	hypotherical prote	leucoanthocyanidin	dioxygenase iron	ethylene-forming e	probable flavonol	gibberellin 20-dio
T09675	T05119	T08008	T10222	S31921	S44261	T47932	C83628	T05551	T06787	T41002	T07972	S47972	T09145	T01606	T06439
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386	356	371	377	365	358	370	320	356	380	321	356	338	298	352	380
7.5	7.4	7.4	7.2	7.2	7.2	7.2	7.1	7.1	7.0	7.0	7.0	6.9	6.9	6.9	6.9
			118.5 7.2												

RESULT 1 T52112 deactoxycephalosporin C synthetase [imported] - Streptomyces clavuligerus C;Species: Streptomyces clavuligerus C;Species: Streptomyces clavuligerus C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 24-Aug-2001 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 24-Aug-2001 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 24-Aug-2001 R;Kovacevic, S; Tobin, M.B.; Miller, J.R. J. Bacteriol. 172, 3952-3959, 1990 J. Bacteriol. 172, 3952-3959, 1990 A;Title: The Detearlactam biosynthetis genes for isopenicillin N epimerase and deacetoxyce A;Recession: T52312 A;Accession: T52312 A;Accession: T52312 A;Status: preliminary; translated from GB/EWBL/DDBJ A;Residues: 1-311 - KOV> A;Residues: 1-311 - KOV> A;Residues: 1-311 - KOV> A;Cross-references: EMBU:M32324; PIDN:AAA26715.1 C;Genetics:	Clusty Match
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Length 311; Query Match
99.5%; Score 1629; DB 2;
Best Local Similarity 99.7%; Pred. No. 4.9e-140;
Matches 310; Conservative 0; Mismatches 1;

ö 1 MDTTVPTESLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE 60 . 0 ò

Indels

	SMGTADNLFPSGDFGRIWT 120		RYFPOVPEHRSAEEOPLRM 180
	61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120	61 AEKRAVISPVPINRRGFIGLESESIAQIINIGSYSDYSMCYSMCTADNLFPSGDFERIWT 120	121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPOVPEHRSAEEOPLRM 180
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240

NYVNIRRTSKA 311 ||||||||||| |NYVNIRRTSKA 311 301 301 ò g

RESULT 2

A32043
deacetoxycephalosporin C synthetase - Streptomyces clavuligerus C, Species: Streptomyces clavuligerus

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C;Species: Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Accession: A39204; A23713
R;Kovacevic, S.; Miller, J.R.
J; Bacteriol. 173, 398-400, 1991
A;Title: Cloning and sequencing of the beta-lactam hydroxylase gene (ceff) from Streptom
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                                                                           243 PKHHVAAPGADKRVGSSRTSSVFFLRPNGDFRFSVPRARECGFDVSIPAETATFDDWIGG 302
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                                                                                                                                                                                                                                                                                                      C;Species: Streptomyces lactamdurans
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 19-May-2000
C;Accession: 840253
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                 A;Residues: 1-310 <COQ>
A;Cross-references: EMBL:221687; NID:g438193; PIDN:CAA79803.1; PID:g438194
A;Cross-references: EMBL:221687; NID:g438193
A;Note: the source is designated as Nocardia lactamdurans
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
                                                            181 APHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGOVKA
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Best Local Similarity 61.2%; Pred. No. 7.8e-80;
Matches 186; Conservative 37; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                          Library, February 1993
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|NYINIRKTAAA 313
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              C; Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 19-May-2000
C; Accession: A32043
R; Kovacevic, S.; Waigel, B.J.; Tobin, M.B.; Ingolia, T.D.; Miller, J.R.
J; Bacteriol. 171, 754-760, 1989
A; Title: Cloning, characterization, and expression in Escherichia coli of the Streptomyd A; Reference number: A32043; MUID:89123150; PMID:2644235
A; Status: preliminary
A; Molecule type: DNA
A; Molecule Lype: DNA
A; Residues: 1-311 < KOV>
C; Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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         13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 19-May-2000
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Pred. No. 7e-100;
41; Mismatches 52; Indels
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Pred. No. 7.5e-140;
1; Mismatches 1;
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Best Local Similarity 99.4%;
Matches 309; Conservative
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Matches
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deacetoxycephalosporin C synthetase - fungus (Acremonium sp.)
Nylternate names: expandase; hydroxylase
Nylternate names: expandase; hydroxylase
C;Species: Acremonium sp.
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 19-May-2000
C;Accession: A29711; A41864
R;Samson, S.M.; Dotalaf, J.E.; Slisz, M.L.; Becker, G.W.; Van Frank, R.M.; Veal, L.E.; Yt
Bio/Technology 5, 1207-1214, 1987
A;Title: Cloning and expression of the fungal expandase/hydroxylase gene involved in cepl
A;Reference number: A29711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 174, 3056-3064, 1992
A.Title: The cefG gene of Cephalosporium acremonium is linked to the cefEF gene and encod
A.Reference number: A41864, MUID:92234966, PMID:1569032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBIP:97574); this ORF is
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56.7%; Pred. No. 2.9e-76;
... winmarches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-332 <SAM>
A;Rote: the source is designated as Cephalosporium acremonium
A;Note: the source is designated as Cephalosporium acremonium
B;Gutierrez, S.; Velasco, J.; Pernandez, F.J.; Martin, J.F.
J. Bacteriol. 174, 3056-3064, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: Strain C10
A;Note: sequence extracted from NCBI backbone (NCBIN:104773, PA;Note: the source is designated as Cephalosporium acremonium C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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A;Status: not compared with conceptual translation
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177; Conservative
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                                                                                                                                                                      Title: Deacetoxycephalosporin C hydroxylase of Streptomyces clavuligerus. Purification; Reference number: A23713; MUID:91161600; PMID:2002049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JACCESSION: S54100
J.Kimura, H.; Izawa, M.; Miyashita, H.; Shimizu, Y.; Sumino, Y.; Suzuki, M.
J.Kimura, H.; Izawa, M.; Miyashita, H.; Shimizu, Y.; Sumino, Y.; Suzuki, M.
J.Danited to the EMBL Data Library, October 1990
J.Description: Gene cluster involved in the cephalosporin biosynthesis from Lysobacter
J.Reference number: S54099
                                                                                                         NID:g153206; PIDN:AAA26716.1; PID:g153207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 PAPRHHVRSPGAGMREGSDRTSSVFFLRPTTDFSFSVAKARSYGLAVDLDMETAFFGDWI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPDRQYTASRAVAREVLRATG---TEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eacetoxycephalosporin C synthetase 1 - Lysobacter lactamgenus (strain YK90)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Lysobacter lactamgenus
\,Variety: strain YK90
};Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
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A.Cross-references: EMBL:X56660; NID:9769806; PIDN:CAA39984.1; PID:9769808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DITVPTESLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKOLVIDFFEHGSEA
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.6%; Pred. No. 1.8e-77;
Matches 180; Conservative 43; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1/Experimental source: strain YK90
;; uperfamily: 1-aminocyclopropane-1-carboxylate oxidase
;; Keywords: antibiotic biosynthesis
                                                                                                                                                                                                                                                                                                                              ,;Gene: cefF
;;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
              Reference number: A39204; MUID:91100311; PMID:1987130
                                                               Molecule type: DNA; Residues: 1-318 <KOV>
; Residues: 1-318 <KOV>
; Acoss-references: GB:M63809; GB:M37186; BAcer, B.J.; Dotzlaf, J.E.; Yeh, W.K.
Biol. Chem. 266, 5087-5093, 1991
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Best Local Similarity 58.0°
Matches 177; Conservative
                                                                                                                                                                                                                                 ;Accession: A23713
;Molecule type: protein
;Residues: 2-29;92-100 <BAK>
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1, Molecule type: DNA
                                            Accession: A39204
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Ribeskiw, B.K.; Amaronowitz, Y.; Mevarech, M.; Wolfe, S.; Vining, L.C.; Westlake, D.W Gene 62, 187-196, 1988

A;Title: Cloning and nucleotide sequence determination of the isopenicillin N synthet A;Feference number: A29894; MUID:88212175; PMID:3130293

A;Accession: A29894
A;Wolfectule type: DNA
A;Residues: 1-329 aLBS>
A;Cross-references: GB:M19421; NID:g153328; PIDN:AAA26770.1; PID:g153329
C;Superfamily: Isopenicillin N synthasse
C;Superfamily: Isopenicillin N synthasse
C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreduct F;48,212,268/Binding site: iron (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces clavuligerus C.Species: Streptomyces clavuligerus C.Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-May-2000 C.Accession: A29894
                                                                                                                                                                                                                                                                                                          67 TDEEKYDLAINAYNKNNPRTRNGY------YMAVKGKKAVESWCYLNPSFSEDHPQI 117
                                                                                                                                                                                                                                                                                                                                                                                                              177 LADTLSAVTLIHYPYLEDYPPVKTGPDGTKLSFEDHLDVSMITVLFQTEVQN----LQVE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 ---FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 -SG---DFGRIW------TQYFDRQYTASRAVAREVLRATGTEPDGGVEA--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 SEABK----RAVTSPVPTMRRGF----TGLESESTAQITWTGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNLFPSGD-----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEA------FLDCE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV 275
                                                                                                                                                                                                 5 VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 VGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VPTFSLAELQQGLHQD-----EPRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                      59 SEAEK----RAVISPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFP--
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Best Local Similarity 23.8%; Pred. No. 4.4e-07;
Matches 77; Conservative 50; Mismatches 150; Indels 46; Gaps
                                                                                                              90;
                                                          Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 329;
F;48,212,268/Binding site: iron (His) #status predicted
                                                    10.8%; Score 176; DB 2; llarity 24.5%; Pred. No. 3.6e-08; Conservative 39; Mismatches 126
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PFVPE-GASEEVRNEALSYGDYL 315
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                                                    Query Match
Best Local Similarity
Matches 73; Conserv
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C,Superfamily: isopenicillin N synthase
C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isopenicillin N synthase (EC 1.14.11.-) pcbC (similarity) - Streptomyces griseus (strain
C,Species: Streptomyces griseus
C,Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 26-May-2000
C,Accession: A61155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Garcia-Dominguez, M.; Liras, P.; Martin, J.F.
Antimicrob. Agents Chemother. 35, 44-52, 1991
A;Title: Cloning and characterization of the isopenicillin N synthase gene of Streptomyd
                                                                                                                                                                                   deacetoxycephalosporin C synthetase 2 - Lysobacter lactamgenus (strain YK90)
C;Species: Lysobacter lactamgenus
C;Variety: strain YK90
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C;Accession: S$4101
R;Kimura, H:/ Izawa, M:/ Miyashita, H:/ Shimizu, Y:/ Sumino, Y:/ Suzuki, M.
submitted to the EMBL Data Library, October 1990
A;Description: Gene cluster involved in the cephalosporin biosynthesis from Lysobacter
A;Accession: S$4099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 2377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 NRMAPHYDLSIVSLILQTPCPNGFVSLQVEIDGRFVEVPPPRPGCVVVFCGSIAPLVSDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X56660; NID:g769806; PIDN:CAA39985.1; PID:g769809
A;Experimental source: strain YK90
C;Superfamily: 1-aminocyclopropae-1-carboxylate oxidase
C;Keywords: antibiotic biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKD----LVIDFFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-329 <GAR>
A;Cross-references: GB:X54609; NID:g509097; PIDN:CAA38431.1; PID:g509098
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              avuligerus.
A;Reference number: A61155; MUID:91197089; PMID:1901702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 852; DB 2;
; Pred. No. 1.6e-69;
48; Mismatches 91;
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301 GNYVNMRRDKPA 312
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Best Local Similarity 52.9°
Matches 165; Conservative
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A;Residues: 1-313 <KIM>
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Riin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84713
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                                                                                                                                                                                                                                                                         194 -----PLKLGPDGEKLSFEHHQDVSLITVLYQTAIPN----LQVETAEGYLDIPVSDE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMC7SWGTAD----N 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 FHEQDSDVRKKFY------TRDVTKTVKYNSNFDLYSSPSANWRDTLS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LFPSGDF------GRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEP- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 CPMAPDVPETEDLPDICGEIMLEYAKRVMKLGELIFELLSEALGLNPNHLKE--MDCTKG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLP 216
--NLFPS----GDFGRIW 119
                                                       -----YMAVEGKKANESFCYLNPSFDADHATIKAGLPSHEVNIWPDEARHPGMRRFY 139
                                                                                                                  TOYFDROYTASRAVAREVLRATGTEPDGGVEAF------LDCEPLLRFRYFPQVPE 169
                                                                                                                                                                            140 EAYPSDVFDVAAVILRGFAIALGRE----ESFFERHFSMDDTLSAVSLIRYPFLENYP- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: GB: AE002093; NID: 93201612; PIDN: AAC20719.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable dioxygenase [imported] - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                       170 HRSAEEQPLRMAP-----HYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPTFSLAELQQGLHQDEF------RRCLRDKGLFYLTDCGLTDTELKSAKDLVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 LLMLSHYYPPCPE----PGLTFGTSPHSDRSFLTILLQ----DHIGGLQVRQNGYWVDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVPGALLVNLGDLLQLMTNDQFVSVEHRVLANK----GEKPRISVASFFVHP 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 146.5; DB 2; Length 362;
; Pred. No. 1.9e-05;
40; Mismatches 118; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                 243 HFLVNCGTYMAHITNGYYPAPVHRV-----KYINAERLSIPFF 280
                                                                                                                                                                                                                                                                                                                                                         221 AVLVFCGAIATLVTGGQVKAPRHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 2
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
   79 GLESESTAQITNTGSYSDYSMCYSMGTAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.9%;
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Best Local Similarity 23.2%
....hes 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary A;Molecule type: DNA
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Subperfamily: isoponicillin N synthase
: Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase
:,45,209,265/Binding site: iron (His) #status predicted
                                                                                                                                                                                                                        .;Title: Nucleotide sequence of the isopenicillin N synthase gene (pcbC) of the gram neg v. Reference number: S08218; MUID:90174998; PMID:2308852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ϋ́Κ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase 45,209,265/Binding site: iron (His) #status predicted
                                                                                      (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .sopenicillin N synthase (EC 1.14.11.-) [similarity] - Lysobacter lactamgenus (strain :).Species: Lysobacter lactamgenus (v.Variety: strain YK90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                          sopenicillin N synthase (EC 1.14.11.-) pcbC [similarity] - Flavobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NLFPS----GDFGRIW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 TQYFDRQYTASRAVAREVLRATGTEPDGGVEAF-----LDCEPLLRFRYFPQVPE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRSAEEQPLRMAP-----HYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPD 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 RACKGSGFFYAANHGV---DLAALQKFTTDWHMAMSPEEKWELAIRAYNPANPRNRNGY- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK----RAVTSPVPTMRRGFT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 RACRGSGFFYAANHGV---DLAALQKFTTDWHMAMSABEKWELAIRAYNPANPRNRNGY- 87
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v;Residues: 1-326 <KIM>
v;Residues: 1-326 <KIM>
v;Cross-references: EMBL:X56660; NID:g769806; PIDN:CAA39983.1; PID:g769807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%; Score 162; DB 2; Length 326; 22.9%; Pred. No. 6.6e-07; tive 34; Mismatches 107; Indels
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                                                                                                                                                                                                        Nucleic Acids Res. 18, 660, 1990
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Matches 65; Conserv
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';Residues: 1-326 <SHI>
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- protein search, using sw model OM protein February 3, 2004, 17:33:57; Search time 42 Seconds (without alignments) 1175.332 Million cell updates/sec Run on:

US-09-582-486-1

1637 1 MDTTVPTFSLAELQQGLHQD.....ATFQDWIGGNYVNIRRTSKA 311 score: Sequence: Perfect

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 segs, 158726573 residues Searched:

1107863 Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
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| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:* A_Geneseq_19Jun03:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Deacetoxycephalosp	S. clavuligerus wi	Streptomyces clavu	Streptomyces clavu	Streptomyces clavu	Streptomyces clavu	S. clavuligerus pe	S. clavuligerus pe	Expandase mutant R
	ID	AAY22220	AAW17775	AAU11044	AAU11050	AAU11046	AAU11051	AAU11053	AAU11525	AAW34168
	DB	20	18	23	23	23	23	23	23	18
	Length	311	311	311	311	311	311	310	310	311
k P	Query ce Match Length DB ID	100.0	99.5	99.5	99.4	99.3	99.3	99.3	99.3	99.3
	Score	1637	1629	1629	1627	1626	1626	1625	1625	1625
	Result No.	-	7	m -	4	ົທັ	, 9	7	80	о

Expandase mutant R	mutant	Streptomyces clavu	Streptomyces clavu	S. clavuligerus mo	Expandase mutant R	Expandase mutant R	Streptomyces clavu	S. clavuligerus pe	Streptomyces clavu	halos	Expandase mutant R	mutant	Expandase mutant P	S. clavuligerus ex	Streptomyces clavu	S. clavuligerus pe	Expandase mutant C	mutan	mutant	utant	S. clavuligerus pe	. clavuligerus	. clavuligerus	. clavuli	. clavuli	. clavuli	S. clavuligerus ex	. clavuligerus							
AAW34176	AAW34175	AAE12016	9	ABG73769	AAW34167	AAW34177	AAU11048	AAU11528	AAU11052	AAP93215	AAW34166	AAW34169		AAW40424	AAU11049	AAU11054	AAU11526	AAU11531	AAU11532	AAU11533	AAU11534	AAU11535	AAW34171	AAW34173	AAW34170	AAW34172	AAU11529	AAU11521	AAU11527	AAW40425	AAW40426	AAW40428	AAW40429	AAU11530	AAW40427
18	18	22	23	24	18	18	23	23	23	10	18	18	18	19	23	23	23	53	23	23	23	23	18	18	18	18	23	23	23	19	19	19	19	23	13
311	311	311	311	311	311	311	311	310	311	311	311	311	311	311	311	309	309	310	310	310	310	310	311	311	311	311	309	308	308	311	311	311	311	308	311
6	99.5	٥.	ø,	6	6	6	ę.	6	ę.	6	9	6	6	ę.	6	6	٩,	ę.	e,	ę.	٩.	٥.	e,	ę.	8	ω.	8	8	œ.	8	æ,	8	œ.	8	8
1625	1624	1624	1624	1624	1623	1623	1623	1622	1622	1621	1621	1621	1621	1621	1621	1620	1620	1620	1620	1620	1620	1620	1620	1620	1619	1619	1617	1616	1616	1616	1615	1614	1614	1613	1612
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39		41	42	43	44	45

ALIGNMENTS

AAY22220 standard; protein; 311 AA Deacetoxycephalosporin C synthase. (first entry) 16-SEP-1999 AAY22220; AAY22220

DAOCS, deacetoxycephalosporin C synthase, antibacterial production; three-dimensional crystal structure; beta-lactam production; penicillin; cephalosporin; cepham; 2-oxoglutarate dependent enzyme; inhibitor; fibrotic disease; liver cirrhosis; arthritis; genetic disorder; therapy; 98GB-0013644. 97GB-0027370. 98WO-GB03860 Streptomyces clavuligerus herbicide resistance. WO9933994-A1. 24-DEC-1998; 24-JUN-1998; 24-DEC-1997; 08-JUL-1999

Baldwin JE, Hajdu J, Harlos K, Lloyd MD; Roach PL, Schofield CJ, Terwisscha Van Scheltinga AS; (ISIS-) ISIS INNOVATION LTD. Andersson I, Ramaswamy S, Valegard K;

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The invention relates to three-dimensional crystal structures of
deacetoxycephalosporin C (DAOC) synthase (DAOCS), which has this amino
acid sequence. Micro-organisms capable of expressing a gene encoding a
caid sequence. Micro-organisms capable of expressing a gene encoding a
conditied DAOCS are useful for the production of beta-lactams of the
penicillin or cephalosporin (including cepham) families. The 3D structure
of DAOCS is used to determine or predict the structure of another related
coorgulusate dependent enzyme (such as deacetylcephalosporin C synthase
CC 2-oxoglutarate dependent enzyme (such as deacetylcephalosporin C synthase)
or related enzymes not from the penicillin and cephalosporin
blosynthesis pathway. The structural data is used to modify the other
corzyme may be prolyl 4/3 or argpartyl/lysyl-hydroxylase and the inhibitor
cervame may be prolyl 4/3 or argpartyl/lysyl-hydroxylase and the inhibitor
cervame may be prolyl 4/3 or argpartyl/lysyl-hydroxylase and the inhibitor desases
including liver cirrhosis and arthritis. The other enzyme may be
p-hydroxyphenylpyruvate dloxygenase and the inhibitor used to tract
certain genetic disorders. Alternatively, the other enzyme is involved in
conditication of the enzyme to accept (or accept more efficiently)
commatural penicillin substrates for the preparation of new or
commercially valuable antibacterials are accept more efficiently)
commatural penicillin substrates for the preparation of new or
commercially valuable antibacterial materials, or to enable the modified
cerzyme to produce unnatural (e.g. exomethylene cephams) or optimise the
production of minor products (e.g. abeta-hydroxycephams) for use as
antibacterials
                                                                                 Three-dimensional crystal structures of deacetoxycephalosporin C synthase useful for the production of beta-lactams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or commercially valuable compounds.
                                                                                                                                                                               Claim 1; Page 11; 178pp; English
                               WPI; 1999-405515/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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100.0%; Score 1637; DB 20; Length 311; 100.0%; Pred. No. 1.1e-172; cive 0; Mismatches 0; Indels 0; Query Match
Best Local Similarity 100.
Matches 311, Conservative

Gaps

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240 AEKRAVISPVPIMRRGFIGLESESTAQIINIGENISSECTSMGTADNLFPSGDFGRIWT 120 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 240 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300 61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120 9 9 1 MDTTVPTFSLAELQQQLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLV1DFFEHGSE NYVNIRRTSKA 311 NYVNIRRTSKA 311 61 121 121 181 181 241 301 301 g В a ઠે 8 ò a 8 g ò ઠે

S. clavuligerus wild type expandase. AAW17775 standard; protein; 311 (first entry) 17-FEB-1998 AAW17775 AAW17775
ID AAW
XX
AC AAI
XX
DT 17
XX
DE S.

RESULT 2

301 NYVNIRRTSKA 311

This sequence represents the wild type expandase from Streptomyces clavuligerus. The DNA encoding this sequence was subjected to site directed mutagenesis to create the mutant expandase sequences of the invention (see AMM34166-W3417). The mutant expandase sequences of the altered substrate specificity compared to the wild type expandase. Expandase catalyses the expansion of the 5-membered thiazolidine ring of penicillin N to the 6-membered dihydrothiazine ring of penicillin N to the 6-membered dihydrothiazine ring of DOAC. The mutant expandase gene is used particularly for the production of 7-aminodesacetoxycephalosporanic acid (7-ADCA). 7-ADCA is one of the key intermediates that is used in the preparation of semi-synthetic cephalosporins. The mutant expandases have improved ability to expand penicillin G into a cephalosporin ring in vitro and/or in vivo where other penicillins such as penicillin N and isopenicillin N can act as Expandase; 7-aminodesacetoxycephalosporanic acid; 7-ADCA production; thiazolidine ring expansion; penicillin N; dihydrothiazine ring; enzyme; semi-synthetic cephalosporin production; penicillin G; isopenicillin N; cephalosporin ring; DOAC. 7-ADCA production; enzymes with mutation(s) to alter substrate specificity Van Der Laan JM; Expandase enzymes with mutation(s) to alused particularly for production of 7-amino:desacetoxy:cephalosporanic acid Disclosure, Fig 1; 21pp; English Bovenberg RAL, Sutherland JD, 95EP-0203259 96WO-EP05358 95US-0007564 Streptomyces clavuligerus (YOX-) UNIV OXFORD. competing substrates. WPI; 1997-310608/28. 311 AA; 27-NOV-1995; 27-NOV-1996; WO9720053-A2 27-NOV-1995; 05-JUN-1997 Sequence

ö 120 61 AEKRAVTSPVPTMRRGFTGLESBSTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWT 120 180 240 240 241 PRHHVAAPRRDQIAGSSRTSSVFILPNADPTFSVPLARECGFDVSLDGETATFQDWIGG 300 121 ÖYFDRÖYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180 241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300 9 9 1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE 1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFBHGSE 61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA Gaps . 0 Query Match 99.5%; Score 1629; DB 18; Length 311; Best Local Similarity 99.7%; Pred. No. 8.5e-172; Matches 310; Conservative 0; Mismatches 1; Indels 0 121 셤 셤 ઠે g 9 8 셤 ò ò à

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121 OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPOVPEHRSAEEQPLRM 180
                                                                                                                                                                                                                                                                                                                                                                              12-MAR-2002
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                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                          AAU11050;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the natural substrate of the unmodified expandase. The invention is substrate of the unmodified expandase. The invention is substrate of the unmodified expandase. The invention is seful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA to produce 7-ADCA, which is useful as a starting point for the production of a range of semi-synthetic cephalosporins, most notably cephalexin. The polymucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a probe. The modification of the penicillin Nexpandase enhances the activity of the enzyme such as penicillin Nexpandase has enhanced catalytic activity or increased specificity for another substrate such as penicillin G. The present protein sequence represents the penicillin Nexpandase enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AEKRAVISPVPTWRRGFIGLESESTAQIINIGSYSDYSMCYSMGTADNLFPSGDFERIWT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRPRYFPQVPEHRSAEEQPLRM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLPPSGDFGRIWT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New enzyme useful for ring-expanding penicillin G to produce phenylacetyl-7-amino desacetoxycephalosporanic acid, comprises penicillin expandase having increased specificity for substrates such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDTIVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                                                                                                                                Streptomyces clavuligerus penicillin N expandase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 311;
                                                                                                                                                                                                                              Penicillin N expandase; ring-expanding; penicillin G;
phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%; Score 1629; DB 23; 99.7%; Pred. No. 8.5e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                       AAU11044 standard; Protein; 311 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-2001; 2001WO-GB02047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-2000; 2000GB-0011185.
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                       Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ACSD-) ACS DOBFAR UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 310; Conservative
301 NYVNIRRTSKA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson RI, Newbert RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-075247/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS17241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as penicillin<sup>G</sup>
                                                                                                                                                                                                                                                                                                                                         WO200185951-A1
                                                                                                                                                           12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                              15-NOV-2001
                                                                                                                         AAU11044;
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                                                    RESULT
                                                                       AAU1104
g
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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the natural_auberTafe of fine unmodified expandase. The invention is not useful for ring-expansion of penicillin of to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA to produce 7-ADCA, which is useful is removed from phenylacetyl-7-ADCA to produce 7-ADCA, which is useful is a starting point for the production of a range of semi-synthetic caphalosporins, most notably cephalexin. The polynucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a producing semi-conformation of the penicillin of or year activity of the enzyme such as penicillin in expandase enhances the activity or increased specificity for another substrate such as activity or increased specificity for another substrate such as claviligenus mutants, AAU11054 and AAU11521-AAU1537, used in the invention to improve the ring-expanding activity of expandase.
                                                                                                      241 PRHHVAAPRRDQIAGSSRTSSVPFLRPNADFTPSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                     181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New enzyme useful for ring-expanding penicillin G to produce phenylacetyl-7-amino desacetoxycephalosporanic acid, comprises penicillin expandase having increased specificity for substrates such as penicillin G -
                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces clavuligerus penicillin N expandase 1305L mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penicillin N expandase; ring-expanding; penicillin G;
phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Ile substituted by Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 AAU11050 standard; Protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page -; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001; 2001WO-GB02047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-2000; 2000GB-0011185.
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ACSD-) ACS DOBFAR UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces clavuligerus.
Synthetic.
                                                                                                                                                                   NYVNIRRTSKA 311
                                                                                                                                                                                                  301 NYVNIRRTSKA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newbert RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-075247/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Misc-difference
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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the neutral substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the production of a range of semi-synthetic cephalosporins, most notably cephalexin. The polymucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a probe. The modification of the penicillin Nexpandase for penicillin G or V as a substrate. The modified expandase has enhanced catalytic activity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, Advilo46-Advilo54 and Advilo51-Advilo57, used in the invention to improve the ring-expanding activity of expandase.

Note: The present protein sequence is not shown in the specification collection of the invention and increased claviligerus wild-type collection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PRHHVAAPRRDQIAGSSRISSVFFLRPNADFIFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPVLRFRYFPQVPEHRSAEEQPLRM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDTTVPTFSLABLQQGLHQDBFRRCLRDKGLFYLTDCGLTDTBLKSAKDLVIDFFBHGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDTTVPTFSLABLQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     penicillin N expandase sequence given in figure 1 (see AAU11044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces clavuligerus penicillin N expandase I305M mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penicillin N expandase; ring-expanding; penicillin G;
phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1626; DB 23;
Pred. No. 1.8e-171;
1; Mismatches 1;
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                                                              Claim 6; Page -; 42pp; English.
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Best Local Similarity 99.4%;
Matches 309; Conservative
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   as penicillin G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 APHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT
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Note: The present protein sequence is not shown in the specification but is derived from the Streptomyces clavuligerus wild-type penicillin N expandase sequence given in figure 1 (see AAU11044).
                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                        Length 311;
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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V; mutant; mutein.
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                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                    Score 1627; DB 23;
Pred. No. 1.4e-171;
1; Mismatches 1;
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                                                                                                                                                                                    Query Match
Best Local Similarity 99.4%;
Matches 309; Conservative
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nyvn<u>i</u>rryska
                                                                                                                            311 AA;
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AAU11046
AAU11046
AAU1104
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Gaps

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Indels

Length 311;

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240

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improve the ring expanding activity for a substrate which is not the natural substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA to produce of semi-synthetic cephalosporins, most notably cephalexin. The polymucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a probe. The modification of the penicillin N expandase enhanced catalytic crivity of the enzyme such as penicillin N expandase has enhanced catalytic crivity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, AAU11046-AAU11054 and AAU11521-AAU1157, used in the invention to improve the ring-expanding activity of expandase.

Note: The present protein sequence is not shown in the specification of but is derived from the Streptomyces clavuligerus wild-type.
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                                                                                                                                                                                                                                                                                                                                               New enzyme useful for ring-expanding penicillin G to produce phenylacetyl-7-amino desacetoxycephalosporanic acid, comprises penicillin expandase having increased specificity for substrates such as penicillin G -
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                 /note= "Wild-type Ile substituted by Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page -; 42pp; English.
                                                                                                                                            09-MAY-2001; 2001WO-GB02047.
                                                                                                                                                                                   09-MAY-2000; 2000GB-0011185.
                                                                                                                                                                                                                             (ACSD-) ACS DOBFAR UK LTD
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Matches 309; Conservative
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301 NYVNMRRTSKA 311
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Misc-difference 305
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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the neutral substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA (canno desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA (canno desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA to produce 7-ADCA, which is useful cephalosporins, most notably cephalexin. The polywuciectide of the invention is useful for producing a primer e.g. a PCR primer and as a provinty of the enzyme such as penicillin a proximate such as penicillin G or V as a substrate. The modified expandase has enhanced catalytic activity of increased specificity for another substrate such as penicillin G or V as a substrate. The modified expandase has enhanced catalytic activity or increased specificity for another substrate such as penicillin C or V as a substrate. The protein sequence is one of a collection of Streptomyces clavuligerus mutants, Abullo46-Abullo54 and Abull521-Abull537, used in the invention to improve the ring-expanding activity of expandase.

C Note: The present protein sequence is not shown in the specification but is derived from the Streptomyces clavuligerus wild-type

    S. clavuligerus penicillin N expandase 1 residue deletion at C-terminus.

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                                                                                                                                                                                                 Penicillin N expandage; ring-expanding; penicillin G;
phenylacetyl-7-ADCA; amino desacetoxycephalosporanic aci
cephalosporin; cephalexin; penicillin V; mutant; mutein.
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Pred. No. 2.3e-171;
0; Mismatches 1;
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                                    AAU11053 standard; Protein; 310 AA
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                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                     Streptomyces clavuligerus
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                                                                                                                    12-MAR-2002
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                                                                             AAU11053;
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the natural substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA to produce 7-ADCA, which is useful as a starting point for the production of a range of semi-synthetic cephalosporins, most notably cephalexin. The polymucleotide of the invention is useful for producing a primer e.g. a PCR primer and as
                                                                                                                            APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                              PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG
          AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT
                                                                                                             APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                            OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Protein is truncated at this residue"
                                                                                                                                                                                                                                                                                                                                                                               clavuligerus penicillin N expandase K310 deletion mutant
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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic aci
cephalosporin; cephalexin; penicillin V; mutant; mutein.
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Misc-difference
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AAU11525
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a probe. The modification of the penicillin expandase enhances the activity of the enzyme such as penicillin N expandase for penicillin G or V as a substrate. The modified expandase has enhanced catalytic activity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, AAU11046-AAU11054 and AAU11521-AAU11537, used in the invention to improve the ring-expanding activity of expandase. Note: The present protein sequence is not shown in the specification but is derived from the Streptomyces clavuligerus wild-type penicillin N expandase sequence given in figure 1 (see AAU11044).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDTTVPTFSLAELQQGLHQDBFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
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Pred. No. 2.3e-171;
0; Mismatches 1;
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Best Local Similarity 99.7%;
Matches 309; Conservative (
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Synthetic.
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27-NOV-1995;
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                                                                                                                                                                 AAW34166-W34177 represent mutant expandase sequences of the invention.

These sequences represent mutated versions of the Streptomyces

Calavuligerus expandase sequences shown in AAW1775. The DNA encoding the

Wild type expandase was subjected to site directed mutagenesis to create

these sequences. The mutant expandase sequences have an altered

Substrate specificity compared to the wild type expandase. Expandase

C atalyses the expansion of the 5-membered thiazolidine ring of penicillin

N to the 6-membered dihydrothiazine ring of DOAC. The mutant expandase

C gene is used particularly for the production of

7-aminodesacetoxycephalosporanic acid (7-ADCA). 7-ADCA is one of the key

Intermediates that is used in the preparation of semi-synthetic

C caphalosporins. These sequences have improved ability to expand

C caphalosporins and a cephalosporin ring in vitro and/or in vivo where

C competing substrates.
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                                                                                           Expandase enzymes with mutation(s) to alter substrate specificity
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                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%; Score 1625; DB 18; Length 311; 99.4%; Pred. No. 2.4e-171; ive 1; Mismatches 1; Indels 0
                                        Van Der Laan JM;
                                                                                                                    7-amino:desacetoxy:cephalosporanic acid
                                                                                                       particularly for production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW34176 standard; protein; 311 AA
                                                                                                                                              Claim 2; Page -; 21pp; English.
                                      Sutherland JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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(KONN ) GIST-BROCADES BV (UYOX-) UNIV OXFORD.
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                                        Bovenberg RAL,
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AAW34166-W34177 represent mutant expandase sequences of the invention. These sequences represent mutated versions of the Streptomyces clavuligerus expandase was subjected to site directed mutagenesis to create wild type expandase sequences substrate specificity compared to the wild type expandase is to create substrate specificity compared to the wild type expandase. Expandase catalyses the expansion of the side thiazolidine ring of penicillin by to the 6-membered dihydrothiazine ring of DOAC. The mutant expandase sequences is used particularly for the production of 7-aminodesacetoxycephalosporant, acid (7-ADCA). 7-ADCA is one of the key intermediates that is used in the preparation of semi-synthetic cephalosporins. These sequences have improved ability to expand penicillin G into a cephalosporin ring in vitro and/or in vivo where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expandase enzymes with mutation(s) to alter substrate specificity used particularly for production of 7-amino:desacetoxy:cephalosporanic acid
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                                                                                                                                                                                                                                         /note= "Arg to Gln mutation"
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                                                                                                                                                                     Location/Qualifiers
cephalosporin ring; DOAC; mutant
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95EP-0203259
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                                                                    Streptomyces clavuligerus
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1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
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                                                                                                                                                                                                           Expandase; 7-aminodesacetoxycephalosporanic acid; 7-ADCA production; thiazolidine ring expansion; penicillin N; dihydrothiazine ring; enzyme; semi-synthetic cephalosporin production; penicillin G; isopenicillin N; cephalosporin ring; DOAC; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expandase enzymes with mutation(s) to alter substrate specificity
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Pred. No. 3e-171;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                     /note= "Arg to Asn mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used particularly for production of 7-amino:desacetoxy:cephalosporanic acid
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                                                                                                  AAW34175 standard; protein; 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .Claim 2; Page -; 21pp; English.
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95EP-0203259.
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                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                 Streptomyces clavuligerus
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                      301 NYVNIRRTSKA 311
    311
                                                                                                                                                                                   Expandase mutant R266N
    NYVNIRRTSKA
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                                                                                                                                                                                                                                                                                                                                      Misc-difference
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Best Local Simi:
Matches 309; (
                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1996;
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27-NOV-1995;
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                                                                                                                                                       17-FEB-1998
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                                                                                                                                                                                                                                                                                                Synthetic
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61 AEKRAVISPVPIMRRGFIGLESESTAQIINIGSYSDYSMCYSMGTADNLFPSGDFERIWT 120
                                                      180
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                                                                                                                                                   241 PRHHVAAPRRDQIAGSSRISSVFFLNPNADFIFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                       PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxygenase; non-haeme iron (II) dependent family; oxidase; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a modified enzyme of a non-haeme iron (II) dependent family of oxygenases and oxidases which renders the enzyme dependent on bicarbonate for activity. The invention also related to a method for producing penicillin G or V comprises employing a modified enzyme, particularly isopenicillin N synthethase (IPNS), in either an organism or a cell-free system, under the control of bicarbonate. The modified enzymes are IPNS, deacetoxycephalosporin C synthetase (DACS) and deacetylcephalosporin C synthetase (DACS) and deacetylcephalosporin C synthetase (DACS) is useful for producing antibiotics, particularly penicillin G or V. The method is useful for making organisms useful for making an antibiotic dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces clavuligerus modified deacetoxycephalosporin C synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method for producing antibiotics, particularly penicillin G or V, comprises employing a modified isopenicillin N synthethase, in either an organism or a cell-free system under the control of bicarbonate –
                                                        OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
                                                                                                                               APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deacetoxycephalosporin C synthetase; DAOCS; antibiotic; penicillin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                  NYVNIRRTSKA 311
                                                                                                                                                                                                                                                                                                           WPI; 2001-615433/71.
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Indels

Conservative

Similarity

MDTTVPTFSLAELQQQLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE

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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the neutural substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the producing a primer e.g. a PCR primer and as a probe. The modification of the penicillin expandase enhances the activity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, Adull046-Adull054 and Adull521-Adull537, used in the present protein sequence is not shown in the specification but is derived from the Streptomyces clavuligerus wild-type.
                                                        Examples; Page -; 42pp; English.
     as penicillin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                                                                                                                                9
on bicarbonate to make the antibiotic. The present sequence is Streptomyces clavuligerus modified deacetoxycephalosporin C synthetase showing an Arg181 in place of Ala181.
                                                                                                                                                                                                                                                                                                1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
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                                                                                                                                                                                                                                                                1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces clavuligerus penicillin N expandase L158A mutant
                                                                                                                                                       99.2%; Score 1624; DB 22; Length 311; 99.4%; Pred. No. 3e-171; 2; Indels 0
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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillín V; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU11047 standard; Protein; 311 AA.
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Synthetic.
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                                                                                                                                                                                  Best Local Similarity 99.4
Matches 309; Conservative
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                                                                                                         311 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-heme iron II dependent family; oxygenase; oxidase; antibiotic; iron ligand; enzyme; bicarbonate; penicillin G; penicillin V; cephalosporin C; isopenicillin N synthetase; IPNS; DAOCS;
penicillin N expandase sequence given in figure 1 (see AAU11044).
                                                                                                                                                                               ó
                                                                                                           Query Match 99.2%; Score 1624; DB 23; Length 311; Best Local Similarity 99.4%; Pred. No. 3e-171; Matches 309; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. clavuligerus modified DAOCS SEQ ID 18
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Synthetic.
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(XONN ) GIST-BROCADES BV. (UYOX-) UNIV OXFORD.
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Matches 309; Conservative
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                                                                                              Key
Misc-difference
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                                                                                                                                                                                                            27-NOV-1996;
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27-NOV-1995;
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                                                                                                                                                                                                                                                                             This invention describes a novel enzyme of a non-heme iron II dependent family of oxygenases and oxidases which is in a pathway to produce an antibiotic. The enzyme comprises a mutation which is an amino acid residue that is two amino acid residues upstream of a histidine residue which is an iron ligand of the enzyme, where the mutation renders the enzyme dependent on bicarbonate to produce the antibiotic. The enzyme and modified organisms containing the enzyme are useful for producing an antibiotic such as peniciallin G or V and cephalosporin C. This sequence represents an deacetoxycephalosporin C synthetase (DAOCS) variant the disclosure of the invention.
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                                                                                                                                                                                                            that renders the
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                                                                                                                                                                                                and
                                                                                                                                                                                                 oxygenases
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 311;
                                                                                                                                                                                            Novel enzyme of non-heme iron II dependent family of oxyge oxidases useful for producing antibiotic, has mutation the enzyme dependent on bicarbonate to produce the antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1624; DB 24; Length
Pred. No. 3e-171;
0; Mismatches 2; Indels
                                                                                                                                       Warner TM,
                                                                                                                                         ν,
                                                                                                                                         Wang
                                                                                                                                                                                                                                                      5; Page 24-25; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.2%;
                                                                                                                                         Kadyrzhanova DK,
                                                       08-AUG-2001; 2001US-0924841.
                                                                                 99US-0413231
                                                                                                             (UNMS ) UNIV MICHIGAN STATE
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Matches 309; Conservative
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                                                                                                                                                                   WPI; 2003-147393/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                      311 AA;
US2002127633-A1
                                                                                 06-OCT-1999;
                           12-SEP-2002
                                                                                                                                         Dilley DR,
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These sequences represent mutated versions of the Streptomyces clavuligerus expandase sequences shown in AAW1775. The DNA encoding the wild type expandase was subjected to site directed mutagenesis to create these sequences. The mutant expandase sequences have an altered substrate specificity compared to the wild type expandase. Expandase catalyses the expansion of the 5-membered thiazolidine ring of penicillin N to the 6-membered dihydrothiazine ring of DOAC. The mutant expandase gene is used particularly for the production of 7-aminodesacetoxycephalosporanic acid (7-ADCA). 7-ADCA is one of the key intermediates that is used in the preparation of semi-seynthetic cephalosporins. These sequences have improved ability to expand penicilling into a cephalosporin ring in vitro and/or in vivo where the remaining such as penicillin N and isopenicillin N can act as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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thiazolidine ring expansion; penicillin N; dihydrothiazine ring; enzyme; semi-synthetic cephalosporin production; penicillin G; isopenicillin N; cephalosporin ring; DOAC; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW34166-W34177 represent mutant expandase sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expandase enzymes with mutation(s) to alter substrate specificity used particularly for production of 7-amino:desacetoxy:cephalosporanic acid
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                                                                                                                                                                                                                                                                                                                                                                       /note= "Arg to Met mutation"
                                                                                                                                                                                                                                                                     Location/Qualifiers
74
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95EP-0203259
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                                                                                                                                                                       Streptomyces clavuligerus
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241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300

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301 NYVNIRRTSKA 311 ||||||||||| 301 NYVNIRRTSKA 311

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Search completed: February 3, 2004, 17:36:36 Job time: 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 3, 2004, 17:33:58; Search time 17 Seconds (without alignments) 860.312 Million cell updates/sec Run on:

US-09-582-486-1 1637 1 MDTTVPTFSLAELQQGLHQD.....ATFQDWIGGNYVNIRRTSKA 311 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	. di	CREB STRCI.	CEFE NOCLA	CEFF NOCLA	CEFF STRCL	EXPA CEPAC	IPNS_STRJU	I PNS STRGR	IPNS_STRCL	I PNS FLASS	I PNS_LYSLA	IPNS STRLP	FLS PETHY	IPNS NOCLA	FLS CITUN	IPNS STRCT	FLS SOLTU	I PNS PENCH	FLS EUSGR	IPNS EMENI	LDOX ARATH	FL3H_DIACA	5		FLS1_ARATH			LDOX MAIZE	LDOX PETHY	LDOX MALDO	FL3H ARATH	FL3H MATIN		FLS_MATIN
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3.4 5.5	36 37 38	6 4 6 0	4 4 4 1 2 6	4 4 5

ALIGNMENTS

RESULT 1

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i E	15-SEP-2003 (Rel. 42, Last annotation update)
DE	phalospori
E C	(Expandase).
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2 0	Streptomyces clavuligetus. Streptomyces clavuligetus.
35	bacterina inclinuarcerina, harrimonarcerinae; harrimoniyoetalee; Attantonuarinasa Attantonuaretarasa Attantonuare
88	NCBI TaxID=1901;
Z.	[1]
RР	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
χX	MEDLINE=89123150; PubMed=2644235;
æ	
RT	"Cloning, characterization, and expression in Escherichia coli of the
RI	Streptomyces clavuligerus gene encoding deacetoxycephalosporin C
RT	synthetase.";
7 S	J. Bacteriol. 171:754-760(1989).
	-!- FUNCTION: CACALYZEB LNE BUED IFOM DENICIAIN N CO GEACELOXY-
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30	OXIDOREDUCTASES. STRONG. TO CEFF.
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ខ្ល	or send an email to license@isb-sib.ch).
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DR.	
DK.	T52312
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Z.	1HJF;
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E E	PDB; 1KKF; 08-JUN-99.
X I	PUB; IKXG; US-UUN-99.
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ž č	PROSTITE: PSOUTHS, TOTAL 1: FALSE NEC
i E	PROSTITE: PS00186: 1PNS 2: 1
. ₹	Antibiotic biosynthesis; Oxidoreductase: Iron: Vitamin C:
K	3D-structure.

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DB 1; Length 314;

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63 AEKKAVMTPIPTIRRGYAGLESESTAQITNTGKYTDYSMSYSMGTADNLFPSAEFEKAWE
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                     InterPro; IPR002057; Isopen_N_synth.
Pfam; PF03171; 20G-FeII Oxy; 1.
PROSITE; PS00185; IPNS_Z; FALSE_NEG.
PROSITE; PS00186; IPNS_Z; FALSE_NEG.
Antibloctic blosynthesis; Oxidoreductase; Iron; Vitamin C. SEQUENCE 314 AA; 34530 MW; D007AD3DE67AlBDF CRC64;
                                                                                                                                                                                                                                                                , Pred. No. 3.6e-102;
41; Mismatches 52;
                                                                                                                                                                                                                                          72.5%; Score 1186.5;
InterPro; IPR005123; 20G-FeII_Oxy
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Matches 217; Conservative
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SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
OXIDOREDUCTASES. STRONG, TO CEFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Gen. Genet. 236:453-458(1993).
FUNCTION: Catalyzes the step from penicillin N to deacetoxy.
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MEDLINE=93173127; PubMed=8437592;
Coque J.J.K., Martin J.F., Liras P.;
Coque J.J.K., Martin J.F., Liras P.;
Characterization and expression in Streptomyces lividans of ceft genes from Nocardia lactamdurans: the organization of the cephamycin gene cluster differs from that in Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cephalosporin C.
CATALYTIC ACTIVITY: Penicillin N + 2-oxoglutarate + O(2)
deacetoxycephalosporin C + succinate + CO(2) + H(2)O.
COFACTOR: Iron and ascorbate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                           Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
1-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Deacetoxycephalosporin C synthetase (EC 1.14.20.1) (DAOCS)
                                                                                                                   Indels
34555 MW; 9C64E1FC37F524BC CRC64;
                                                        Score 1629; DB 1;
Pred. No. 4.4e-143;
0; Mismatches 1;
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                                                        99.5%;
al Similarity 99.7%;
310; Conservative
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   311 AA;
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                      123 DYFARMYRASQDVARQVLTSVGAEPEVGMDAFLDCEPLLRIRYFPEVPEDRVAEEQPLRM
                                                                                                          121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
                                                                                    181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Deacetoxycephalosporin C hydroxylase (EC 1.14.11.-)
(Deacetylcephalosporin C synthetase) (DACS) (Beta-lactam hydroxylase)
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-!- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
OXIDOREDUCTASES. STRONG, TO CEFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96287477; PubMed=8703431;
Coque J., Enguita F.J., Cardoza R.E., Martin J.F., Liras P.;
"Characterization of the ceff gene of Nocardia lactamdurans a 3'-methylcephem hydroxylase different from the 7-cephem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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-!- FUNCTION: HYDROXYLATION OF DESACETOXICEPHALOSPORIN C
3'POSITION TO FORM DEACETYLCEPHALOSPORIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis
NCBL_TaxID=1913;
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EMBL; Z13974; CAA78376.1; -.

PIR; S30900; S30900

us-09-582-486-1.rsp

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PIR; A39204; A39204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 NHHVVSPDASMLKGSDRTSSVPFLRPSTDFTFSVPDARKYGLDVSLDMEKATFGDWIGTN 301
                                                                                                                                                                                                                                                                                                                                                                  EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                  EKQAVTTKVPTMRRGYSALEAESTAQVTNTGTYTDYSMSYSMGIGGNLFPSKEFESVWTD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMA 181
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                                                                                                                                                                                                                                                                   DTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Deacetoxycephalosporin C hydroxylase (EC 1.14.11.-)
(Deacetylcephalosporin C synthetase) (DACS) (Beta-lactam hydroxylase)
CEPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91100311; PubMed=1987130;

Kovacevic S., Miller J.R.;

"Cloning and sequencing of the beta-lactam hydroxylase gene (ceff)
from Streptomyces clavuligerus: gene duplication may have led to
separate hydroxylase and expandase activities in the actinomycetes.";
J. Bacteriol. 173:398-400(1991).
-I- FUNCTION: HYDROXYLATION OF DESACETOXICEPHALOSPORIN C IN
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'POSITION TO FORM DEACETYLCEPHALOSPORIN C. PATHWAY: CEPPALOSPORIN DIOSPYTATHORIS. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES. STRONG, TO CEFE.
                                                                                                                                                                                                                    ï
                                                                                                                                                                    Query Match 59.0%; Score 965.5; DB 1; Length 310; Best Local Similarity 61.2%; Pred. No. 9.4e-82; Matches 186; Conservative 37; Mismatches 80; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
EMBL; Z21687; CAA79803.1; -.
PIR; S40253; S40253.
InterPro; IPR005123; 20G-FeII Oxy.
Pfam; PP03171; 20G-FeII Oxy; I.
Antiblotic blosynthesis; Oxidoreductase; Iron; Vitamin C.
SEQUENCE 310 AA; 34364 MW; 9983EFIACIB416E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1901;
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CEFF_STRCL
TO CEFF_STRCL
DT 01-NOV-
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DE Deacett
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122 YFDRQYTASRAVAREVLRATG----TEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPL 178
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                                                                                                                                                                                                                                                                                          62 EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cephalosporíum acremoníum (Acremoníum chrysogenum).
Eukaryota, Fungi, Ascomycota, Pezizomycotina; Sordariomycetes;
Hypocreomycetidae, Hypocreales; Hypocreaceae; mitosporic Hypocreaceae;
                                                                                                                                                                                                                                2 DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 KAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWI
                                                                                                                                                        Gaps
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01-0CT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cephalosporin biosynthesis expandase/hydroxylase [Includes: Deacetoxycephalosporin C synthetase (EC 1.14.20.1) (DACCS) (Expandase); Deacetoxycephalosporin C hydroxylase (EC 1.14.11.-) (Deacetylcephalosporin C synthetase)
                                                                                                                                                      3;
                                                                                                        Length 318;
InterPro; IPR005123; 20G-FeII Oxy.
Pen; PF03111; 20G-FeII Oxy; 1.
Antibioto biosysis; Oxidoreductase; Iron; Vitamin C.
SEQUENCE 318 AA; 34584 MW; B17CCICBCIE67178 CRC64;
                                                                          57.4%; Score 939.5; DB 1; Pred. No. 2.5e-79; "... Pred. No. 2.5e-79; "... "... 81;
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InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 20G-FeII_Oxy; I.
                                                                                                                                 Best Local Similarity 58.6
Matches 180; Conservative
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SEQUENCE
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                                                                                                                                                                                          61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120
                                                                                                                                                                                                               61 EEKRAVTLADRNARRGFSALEWESTAVVTETGKYSDYSTCYSMGIGGNLFPNRGFEDVWQ 120
                                                                                                                                                                                                                                     OYFDROYTASRAVAREVLRATGTEPDG-GVEAFLDCEPLLRFRYFPOVPEHRSAEEQPLR 179
                                                                                                                                                                                                                                                 121 DYFDRMYGAAKDVARAVLNSVGAPLAGEDIDDFVECDPLLRLRYFPEVPEDRVAEEFPLR 180
                                                                                                                                                                                                                                                                                180 MAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVK 239
                                                                                                                                                                                                                                                                                           APRHHVAAPRRDOIAGSSRISSVFFLRPNADFIFSVPLARECGFDVSLDGETATFQDWIG 299
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                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin synthetase)
                                                                                                . Match 56.6%; Score 926.5; DB 1; Length 332; Local Similarity 56.7%; Pred. No. 4.2e-78; les 177; Conservative 43; Mismatches 91; Indels 1.
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MUTAGENESIS OF HISTIDINE AND ASPARTIC ACID RESIDUES.
MEDLINE=96229923; PubMed=8639682;
Borovok I., Landman O., Kreisberg-Zakarin R., Aharonowitz Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces jumonjinensis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
PROSITE; PS00185; IPNS_1; 1.
PROSITE; PS00186; IPNS_2; 1.
Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin (Multfunctional enzyme.
METAL 184 184 IRON (BY SIMILARITY).
METAL 244 IRON (BY SIMILARITY).
SEQUENCE 332 AA; 36479 MW; E0BD&CE68AA28B79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1945;
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                                                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VPTFSL-----AELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTBLKSAKDLVIDFFBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 -NLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCE----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 LIRYPYLEEYPPVKTGADGTKLSFEDHLDVSMITVLYQTEVQN----LQVETVDGWQDIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Gaps
rainwar: Blosynthesis of penicillin and cephalosporin.
SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY
OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q54243;
15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 YRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
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STRAIN=NRRL 3851;
MEDLINE=91197089; PubMed=1901702;
Garcia-Dominguea M., Liras P., Martin J.F.;
"Cloning and characterization of the isopenicillin N synthase griseus NRRL 3851 and studies of expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSDEDFLVNCGTYMGHITHDYFPAPNHRV-----KFINAERLSLPFFL 284
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1911;
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InterPro; IPR002123; 2OG-FeII Oxy.
InterPro; IPR002283; IPN synth.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 2OG-FeII Oxy; 1.
PRINTS; PR00682; IPNSYTHASE.
PROSTIE; PS00186; IPNS 1; 1.
PROSTIE; PS00186; IPNS 1; 1.
Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin
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329 AA; 37305 MW; 9C8F1EB8FB8DFC6
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 RSGTPWHEGNIWPDEKRHQRFRPFCEQYYRDVFSLSKVLMRGFALALG-KPEDFFDASLS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SG---DFGRIW------TQYFDRQYTASRAVAREVLRATGTEPDGGVEA--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 VPIIDISPLSGGDADDKKRVAQEINKACRESGFFYASHHGI---DVQLLKDVVNEFHRTM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 VGGAFIDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 TADGWQDLPTSGENFLVNCGTYMGYLTNDYFPAPNHRV-----KFINAERLSLPFFL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEAEK-----RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPTFSLAELQQGLHQD-----EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
         claviligerus.";
Antimicrob. Agente Chemcher. 35:44-52(1991).
-!- FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delter. (acrieve of oxygen, 4 hydrogen atoms from the azeridinone and thiazolidine rings of isopenicillin.
-!- CATALYTIC ACTIVITY: N- ([58)-5-amino-5-carboxypentanoy]: L-cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.
-!- COFACTOR: Iron and ascorbate.
-!- PATHMAY: Bicosyntheeis of penicillin and cephalosporin.
-!- SIMILARIY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
18openicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 176; DB 1; Length 325
24.5%; Pred. No. 9.7e-09;
tive 39; Mismatches 126; Indels
complementation of the cephamycin pathway in Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                    212 212 IRON (BY SIMILARITY).
214 214 IRON (BY SIMILARITY).
268 268 IRON (BY SIMILARITY).
329 AA; 37368 MW; 0CD96C8F7CF5A7EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin
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InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR012057; Isopen N synth.
Pfam; PF01311; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00186; IPNS 1; 1.
PROSITE; PS00186; IPNS 2; 1.
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HSSP; P05326; 1BK0.
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nes 73; Conserv
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P10621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 TDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDHPM-IAAGTPMHE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 VNLWPDEERHPRFRPFCEGYYROMLKLSTVLMRGLALALG-RPEHFFDAALAEQDSLSSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 PTSENDFLVNCGTYMAHVTNDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV
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                                                                                                                                                                                                                               Leskiw B.K., Aharonowitz Y., Mevarech M., Wolfe S., Vining L.C., Westlake D.W.S., Ganneen S.E., "Cloning and nucleotide sequence determination of the isopenicillin synthetase gene from Streptomyces clavuligerus.";
                                                                                                                                                                                                                                                                                                                                                                                              Gene 62:187-196 (1988).

-!- FUNCTION: Removes, in the presence of coxygen, 4 hydrogen atoms from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.
-!- CATALYTIC ACTIVITY: N-[(58)-5-amino-5-carboxypencanoyl]-L-cysteinyl-D-valine + 0(2) = isopenicillin N + 2 H(2)0.
-!- PATHWAY: Biosynthesis of penicillin and cephalosporin.
-!- PATHWAY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        doreductase, Iron, Vitamin
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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Streptomycineae, Streptomycetaceae, Streptomyces.
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                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE=88212175; PubMed=3130293;
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InterPro; IPR002283; IPN SYMEN.
InterPro; IPR002057; Isopen N symth.
Pfam; PF03171; 2OG-FeII Oxy; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 268 II
329 AA; 36958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEGM; PF03171; 20G-FeII OXY;
PRINTS; PR00682; IPNSYNTHASE.
PR051TB; PS00185; IPNS_1; 1.
PR05ITE; PS00186; IPNS_2; 1.
Antiblotic blosynthesis; Oxid
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                             -HYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPD 220
                                                                                      -----PLKLGPDGEKLSFEHHQDVSLITVLYQTAIPN----LQVETAEGYLDIPVSDE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRRGFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthesis from Lysobacter lactamgenus Yk90.";
Appl. Microbiol. Biotechnol. 44:589-596(1996).
-!- FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.
-!- CATALYTIC ACTIVITY: N- [(SS)-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + 0(2) = isopenicillin N + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimura H., Izawa M., Sumino Y., "Molecular analysis of the gene cluster involved in cephalosporin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- PATHWAY: Biosynthesis of penicillin and cephalosporin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lysobacter lactamgenus.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                         221 AVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                     243 HFLVNCGTYMAHITNGYYPAPVHRV-----KYINABRLSIPFF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Mismatches 107; Indels
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PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00186; IPNS_1; 1.
PROSITE; PS00186; IPNS_2; 1.
Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin
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HSSP, POSJGG, IBKO.
InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002033; IPN synth.
InterPro; IPR002057; Isopen N synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=YK90;
MEDLINE=96287475; PubMed=8703429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
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                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                          170 HRSAEEQPLRMAP-
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326 AA;
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es 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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LYSLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NLFPS----GDFGRIW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YMAVEGKKANESFCYLNPSFDADHATIKAGLPSHEVNIWPDEARHPGMRRFY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 TQYFDRQYTASRAVAREVLRATGTEPDGGVEAF-----LDCEPLLRFRYFPQVPE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 BAYPSDVFDVAAVILRGFAIALGRE----ESFFERHFSMDDTLSAVSLIRYPFLENYP- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RACRGSGFFYAANHGV---DLAALQKFTTDWHMAMSAEEKWELAIRAYNPANPRNRNGY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=90174998; PubMed=2308852;
Shiffman D., Cohen G., Aharonowitz Y., von Dohren H., Kleinkauf H.,
Mevarech M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the isopenicillin N synthase gene (pcbC) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Gram-negative Flavobacterium sp. SC 12,154.";

Nucleic Acids Res. 18:660-660(1990).

-!- FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.

-!- CATALYTIC ACITUTY: N [(58)-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.

-!- COFACTOR: Iron and ascorbate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Biosynthesis of penicillin and cephalosporin. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Flavobacterium sp. (strain SC 12,154).
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 1; 1
1.9e-07;
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                                                                                                                                                            326 AA.
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22.9%; Pred. No. 1
294 PFVPE-GASEEVRNEALSYGDYL 315
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InterPro; IPR002283; IPN synth.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 20G-FeII Oxy; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flavobacteriaceae; Flavobacterium
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                                                                                                              170 HRSAEEQPLRMAP-----HYDLSMVTLIQQIPCANGFVSLQAEVGGAFTDLPYRPD 220
                                                                                                                               194 -----PLKLGPDGEKLSFEHHQDVSLITVLYQTAIPN----LQVETAEGYLDIPVSDE 242
GLESESTAQITNTGSYSDYSMCYSMGTAD------NLFPS----GDFGRIW 119
                          -----YMAVEGKKANESFCYLNPSFDADHATIKAGLPSHEVNIWPDEARHPGMRRFY 139
                                                                                  140 EAYFSDVFDVAAVILRGFALALGRE----ESFFERHFSMDDTLSAVSLIRYPFLENYP- 193
                                                       TQYFDRQYTASRAVAREVLRATGTEPDGGVEAF------LDCEPLLRFRYFPQVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nidulans.",
J. Bacteriol. 170:3817-3826(1988).

J. Bacteriol. 170:3817-3826(1988).

I. Bacteriol. 170:3817-3826(1988).

I. FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delte.L.(alpha-aminoadipyl).L.-cysteinyl.-D.valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.

I. CATALYTIC ACTIVITY: N. [(58)-5-amino-5-carboxypentanoyl].L.-cysteinyl. D-valine + 0(2) = isopenicillin N + 2 H(2)0.

I. CAFATOR: Iron and ascorbate.

I. PATHWAY: Biosynthesis of penicillin and cephalosporin.

I. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF AvenoPendTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=88314868; PubMed=3045077; Weigel B.J., Burgett S.G., Chen V.J., Skatrud P.L., Frolik C.A. Queener S.W., Ingolia T.D.; "Cloning and expression in Escherichia coli of isopenicillin N synthetase genes from Streptomyces lipmanii and Aspergillus
                                                                                                                                                                                                                                                                                                    01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                         243 HFLVNCGTYMAHITNGYYPAPVHRV-----KYINAERLSIPFF 280
                                                                                                                                                                       221 AVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin C.
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IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces lipmanii (Streptomyces alboniger)
                                                                                                                                                                                                                                                                          333 AA.
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InterPro; IPR002283; IPN synth.
InterPro; IPR012057; ISOpen_N synth.
Pfam, PF01171; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00188; IPNS 1; 1.
PROSITE; PS00186; IPNS 1; 1.
                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=132472;
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                                                                                                                                                                                                                                                                                                                                                            synthase).
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286
                                                                                                                                                                                                                                                                                           58 GSEAEK----RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCY---SMGTADNL 109
                                                                                                                                                                                                                                                                                                                                                                        66 MTDQEKHDLAIHAYNENNSHVRNGY-----YMARPGRKTVESWCYLNPSFGEDHPM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                             110 FPSG-----EPDGTIWTQYFDRQYTASRA-VAREVLRATGT-----EPDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 IKAĞTPMHEVNVWPDEERHPDPRSPGEQYYREVFRLSKVLLLKGFALALGKPEEFFENEV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GVEAFLDCEPL-LRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 LQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
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MEDLINE=94108485; PubMed=7904213;
MEDLINE=94108485; PubMed=7904213;
MEDLINE=94108485; PubMed=7904213;
MICTONI CATALYZES FOR THE FORMATION OF FLAVONOLS FROM
DIHYDROFLAVONOLS. IT CAN ACT ON DIHYDROKAEMPFEROL TO PRODUCE
KAEMPFEROL, ON DIHYDROURREFIN TO PRODUCE QUERCITIN AND ON
DIHYDROMYRICETIN TO PRODUCE MYRICETIN.
-!- CORCIOR: IRON AND ASCORBATE.
-!- PATHWAY: PART OF THE BLOSYWHHETIC PATHWAY FOR FLAVONOLS WHICH ARE
FLAVONOLDS. FLAVONOLS ARE IMPORTANT CO-PIGMENTS IN FLOWER OF FRUIT
COLOR AND ARE ALGO ESSENTIAL FOR POLLEN TUBE GROWTH.
                                                                                                                                                                                        10 VPIIDISPL-FGTDPDAKAHVARQINEACRGSGFFYASHHGI---DVRRLQDVVNEFHRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VPTPSLAELQQGLHQD-----EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 LÓVETVDGWOSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNABRLSLPP
                                                                        64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic.
DEVELOPMENTAL STAGE: EXPRESSED AT HIGHEST LEVEL DURING THE FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, lamids, Solanales, Solanaceae, Petunia.
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   Length 333;
                                                                        37; Mismatches 131; Indels
8.7%; Score 143; DB 1; 23.2%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
16-077-2001 (Rel. 40, Last annotation updat
Flavonol synthase (EC 1.14.11.-) (FLS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAGE OF FLOWER DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petunia hybrida (Petunia).
Query Match
Best Local Similarity 23.2%
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Similarity
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SEQUENCE FROM N.A.
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Best Local S
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FLS_CITUN
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                                                                                                                                                                                                                               85 TAQITUTGSYSDYSMCYSMGTADNLF-----PSGDFGRIW-------TQYFDRQYT 128
                                                                                                                                                                                                                                                                                                                                         129 ASRAVAREVLRATGTEPDGGVEAFLDCE--PLLRFRYFPQVPEHRSAEEQPLRMAPHYDL 186
                                                                                                                                                                                                                                                                                                                                                                       182 VVDRIFKSLSLGLGLEGHEMIEAAGGDEIVYLKINYYPPCPR----PDLALGVVAHTDM 237
                                                                                                                                                                                                                                                                                                                                                                                                       SMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVA 246
                                                                                                                                                                                                                                                                                                                                                                                                                           137 EGK------KGWVDHLFHKIWPPSAVNYRYWPKNPPSYREANEEYGKRMRE 181
                                                                                                                                                                                                              84
                                                                                                                                                                                                            RDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVT-SPVPTMRRGF-TGLESES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=VAR LC 411;
MEDLINE=22065008; PubMed=1956290;
Coque J.J.R., Martin J.F., Calzada J.G., Liras P.;
Coque J.J.R., Martin J.F., Calzada J.G., Liras P.;
The cephamycin biosynthetic genes pcbAB, encoding a large multidomain peptide synthetase, and pcbC of Nocardia lactamdurans are clustered together in an organization different from the same genes in Acremonium Chrysogenum and Penicillium chrysogenum.";
Mol. Microbiol. 5:1125-1133(1991).
                                                                                              ပ
                            InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR012283; IPN synth.
Pfam; PF03171; 20G-FeII Oxy; 1.
PRINTS; PR00682; IPNSYNTHASE.
Flavonoid biosyntheeis; Oxidoreductase; Dioxygenase; Iron; Vitamin SEQUENCE 348 AA; 39427 MW; B39EIE4381DE6379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (AcV) to form the azetidinone and thiazolidine rings of isopenicillin. CATALYTIC ACTIVITY. N-([58]-5-amino-5-carboxypentanoyl]-L-COPACTOR: Iron and ascorbate.

PATHWAY: Biosynthesis of penicillin and cephalosporin.

SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IRNS) (Isopenicillin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                           8.6%; Score 140; DB 1; Length 348; 22.3%; Pred. No. 2.2e-05; iive 43; Mismatches 114; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 APRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 VNK-----DKTRMSWPVFLEPPSE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
Z22543; CAA80264.1; -.
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nocardia lactamdurans
                PIR; S33510; S33510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OXIDOREDUCTASES
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1913;
                                                                                                                                                                            59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthase).
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                                                                                                                                              Query Match
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Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                          65 SPQEKYDLAIHAYNKNNSHVRNGYYMAIEGKKAVE-----SFCYLNPSFSEDHPE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                      102 -SMGT---ADNLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGT-----EPDGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 VEAFLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 BADTLSSVSLIRYPYLEDYPPVKTGPDGEKLSFEDHFDVSMITVLYQTQVQN----LQVE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 IKAGTPMHEVNSWPDEEKHPSFRPFCEEYYWTMHRLSKVLMRGFALALGKDERFFEPELK 174
                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 VGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 TVDGWRDLPTSDTDFLVNAGTYLGHLTNDYFPSPLHRV-----KFVNAERLSLPFF 281
                                                                                                                                                                                                                                                                                                                         5 VPTFSLABLQQGLHQD-----EFRRCLRDKGLFYLTDCGLTDTBLKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                            59 SEAEK----RAVTSPVPTMRRG-FTGLESESTAQITNTGSYSDYSMCY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Citrus unshiu (Satsuma orange).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                               90;
                                            Length 328;
                                                                                                                                                                                                                                                                                             41; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Flavonol synthase (EC 1.14.11.-) (FLS) (CitFLS)
                                                                                                                                                                                                                                                                     8.4%; Score 138; DB 1; 22.6%; Pred. No. 3.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Satsuma Mandarin;
PubMed=11903972;
                                        EMBL; X57310; CAA40562.1; -
                                                                                                                                                                                                                                                                                               67; Conservative
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            102 VYSRPADA--KDVQGYGTKLQKEVEGKKSWVDHL---------FHRVWPPSSI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 NYRFWPKNPPSYRAVNEEYAKYMREVVDKLFTYLSLGLGVEGGVLKEAAGGDDIEYMLKI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYYPPCPR----PDLALGVVAHTDLSALTVL----VPNEVPGLÖVFKDDRWIDAKYIPNA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --QYFDRQYTASRAVAREVLR------ATGTEPDGGV--EAF--LDCEPLLRF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDA 221
                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                            43 IPTIDLDDPVODRLVRSIAEASREWGIFOVTNHGIPSDLICKLOAVGKEFFELPOE-EKE 101
                                                                                                                                                                                                                                                                                                                                                                   5 VPTPSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKR
                                                                                                                                                                                                                                                                                                                                                                                                                         AVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT----
           TISSUE SPECIFICITY: In the juice sacs/segment epidermis (edible part) at the early developmental stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005123; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy; 1.
Flavonoid biosynthesis; Oxidoreductase; Dioxygenase; Iron; Vitamin SEQUENCE 335 AA; 37899 MW; 157EIAFA4C47564B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     loning and sequencing the isopenicillin N synthetase (IPNS) gene
                                                       maturation.
SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1sopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 VLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVIHIGDQIEILSNGKYKAVLHRTTVNK-----DKTRMSWPVFLEPPAD 299
                                                                                                                                                                                                                                                                                                            DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                        DEVELOPMENTAL STAGE: Increases in the peel during fruit
                                                                                                                                                                                                                                                                                                         8.4%; Score 137.5; DB 1; Length 21.8%; Pred. No. 3.6e-05; tive 47; Mismatches 124; Indels
 SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomycineae, Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97350503; PubMed=9206271;
                                                                                                                                                                                                                         EMBL; AB011796; BAA36554.1; -.
                                                                                                                                                                                                                                                                                                                       Local Similarity 21.8 tes 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces cattleya.
                                                                                 OXIDOREDUCTASES
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Q53932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 KAGTPMHEVNVWPDEERHPDFGSFGEQY-HREVSASRRCCCGASRWRRQAGESSSNEVTE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 EVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PSG-----AREVLRATGTEPDGGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQ----ITNTGSYSDYSMCY---SMGTADNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ----ESTIMIDQRSIIWRSIRYNENNSHVRNGYYMARPGREIVESWCYLNPSFGEDHPMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 EAFLDCEPLLRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 EDTLSAVSMIRYPYLDPYPEAAIKTGPDGTRLSFEDHLDVSMITVLSKTEVQN----LQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 ETVDGWQSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPFFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S VPTFSLAELQQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 VPTIDISPQLPGTDPTPRRTSRGRSTRPARGSGPPYASHHGIDVRRLQTWSN------
                           PATHWAY: Biosynthesis of penicillin and cephalosporin. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36576 MW; BCCOCFFCF7C07AF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.4%; Score 137; DB 1; 3.1%; Pred. No. 3.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005123; 2OG-FeII Oxy.
InterPro; IPR002283; IPW Synth.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; ZOG-FeII_OXy; I.
COFACTOR: Iron and ascorbate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 PNADFTFSVPLARECG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 AGONSVMK-PFTRRTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROOG82; IPNSYNTHASE.
PROSITE; PSO0185; IPNS_1; 1.
PROSITE; PSO0186; IPNS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D78166; BAA11234.1; -.
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269
321 AA;
                                                                                            OXIDOREDUCTASES
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tes 73; Conserv
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SEQUENCE
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Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Q9fab9 streptomyce
Q91r25 streptomyce
Q81r25 oryza sativ
Q80851 arabidopsis
Q80850 arabidopsis
Q80850 arabidopsis
Q80850 arabidopsis
Q941p7 oryza sativ
Q39112 arabidopsis
Q9fsy streptomyce
Q91144 arabidopsis
Q9fsy streptomyce
Q91if4 arabidopsis
Q9fsy streptomyce
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Q8lby oryza sativ
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Deacetoxycephalosporin C synthase.
Streptomyces jumonjinensis.
Bacteria; Actinobacteria; Actinobacteria, Actinobacteria; Actinobact
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SEQUENCE FROM N.A.
SIM T.S., Sim J.;
Cloning and purification of Streptomyces jumonjinensis
deacetcxycephalosporin C synthase.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF317908, AAL09460.1, -.
InterPro; IPR005123; 20G-FeII_0xy.
InterPro; IPR005127; Isopen_N_gynth.
Pfam; PP03117; 20G-FeII_0xy;
Pfam; PP03117, 20G-FeII_0xy;
I. 20G-FeII_0xy.
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(c) 1993 - 2004 Compugen Ltd.
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                                                                                     APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
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MEDLINE=96287475; PubMed=8703429;
Kimura H., Izawa M., Sumino Y.;
Kimura H., Izawa M., Sumino Y.;
"Molecular analysis of the gene cluster involved in cephalosporin biosynythesis from Lysobacter lactamgenus YK90.";
pppl. Microbiol. Biotechnol. 44:589-596(1996).
EMBL; X5660; CAA39984.1; -
InterPro; IRN05123; 20G-FeII_Oxy.
Pfam; PF03171; 20G-FeII_Oxy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lysobacter lactamgenus.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Lysobacter.
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58.0%; Pred. No. 3.5e-79;
ive 45; Mismatches 83; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          319 AA
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Best Local Similarity 58.0°
Matches 177; Conservative
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01-NOV-1996
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RESULT

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61 EEKRAVTLADRNARRGFSALEWESTAVVTETGKYSDYSTCYSMGIGGNLFPNRGFEDVWQ 120
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                                                                                                                                                                                                                                                                                                                               Jekosch K., Nosek J., Kueck U.;
"Analysis of cefEF gene expression in two cephalosporin C producing strains of Acremonium chrysogenum.";
Submitted (JUL-2000) to LHE EMBL/GenBank/DDBJ databases.
EMBL, AJ404737; CAB96750.1;
InterPro; IPR00123; 20G-FeII_Oxy.
InterPro; IPR002017; Isopen. N synth.
PROSITE; PS00185; IPNS 1; 1.
PROSITE; PS00186; IPNS 1; 1.
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                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Hypocreales, Hypocreaceae, Acremonium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E3DEECE5E9C28B79 CRC64;
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                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                  Cephalosporium acremonium (Acremonium chrysogenum)
                                       01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence updat
01-0tN-2002 (TrEMBLrel. 21, Last annotation upd
01-ottylcephalosporin C synthetase/hydroxylase.
CEFEF.
332
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PRT;
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NCBI_TaxID=39596;
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PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=YK90;
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Best Local Similarity
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Kimura H., Izawa M., Sumino Y.; Molecular analysis of the gene cluster involved in cephalosporin biosynythesis from Lysobacter lactamgenus YK90."; Appl. Microbiol. Biotechnol. 44:589-596(1996). "Biotechnol. Hiotechnol. 14:589-596(1996). "InterPro: IPRO5123; ZOG-Pell. Oxy. Pfam; PF03171; ZOG-Pell.Oxy; I.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                             52.0%; Score 852; DB 2; Length 313; 52.9%; Pred. No. 3e-71;
                                                                                                                                                                                                                                                                                                                   91; Indels
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                                                                                                                                                                                                          313 AA; 34418 MW; 4C341A6FFE771CD6 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                        ; Pred. No. 3e-7
48; Mismatches
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InterPro; IPR005123; 20G-F011 Oxy.
InterPro; IPR002283; IPN synth.
Pfam; PF03171; 20G-F011 Oxy; 1.
PRINTS; PR00682; IPNSYNTHASE.
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01-JUN-2002
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                                                                                                                                                                                                            SEQUENCE
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10.3%; Score 168; DB 16; Length 366;

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                                                                                                                                                                                                                                                                                                                                                                                                                249 SWYDVDPIPGTLVVNIGELLELASNGYLRATVHRVVTPP----AGVERISVPFFFSARLD 304
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                                                                                                                                                                                                                                                                                                88 AL-PEADKLAIEMVKSSQFRGYTRAGGELTK-----GREDWREQLDIGVERQAIAQGPG 140
                                                                                                                                                                                                                                                                                                                                                                      116 GRIWTQ-YFDRQYTAS-------RAVAREVLRATGTEPDGGVEAFLDCEPLL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 ----YSSEPNHRMKIVRYPGRDTTGGDQGVGAHKDGGFLTLLLQ----DDNKGLQVDYDG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 AFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 SEAEK-----RAVISPVPTMRRG-FTGLESESTAQITNTGSYSDYSMCY---SMGTADNL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEA-- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=JCM 4910; Sim T.S., Yo C.Y., Wong B.; Sim T.S., Yo C.Y., Wong B.; "Genome walking and PCR-based cloning of isopenicillin N synthase gene
                                                                                                 1 MDTTVPTFSLAELQQGLHQ-----DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 RFRYFPQVPEHR-SAEEQPLR-----MAPHYDLSMVTLIQQTPCANGFVSLQAEVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VPTFSLABL-----QQGLH-QDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VPTIDISPLFGDDPDAKTHVAQQINKACRGSGFFYASHHGI----DVQQLQDVVNEFHGTM
                                                                                                                                                         28 MPRIVPVLDLSRLEQGASERRTFLADLRSASRDIGFFYLAGHGISWAEISBVLTASRQFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.8%; Score 161; DB 2; Length 329;
Best Local Similarity 23.4%; Pred. No. 1.2e-06;
Matches 70; Conservative 42; Mismatches 125; Indels 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=68197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 FT----FSVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 ATIPLIGLSEELAAQARGPAS-DPDNPLFRD-VGTNVLKSRLRS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Streptomyces fimbriatus.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF320779; AKK1117.1;
INSEPP: P05326; 1BLZ.
InterPro; IPR005123; 2OG-FeII Oxy.
InterPro; IPR00253; IPW synth.
InterPro; IPR002057; Isopen W synth.
PF03171; 2OG-FeII Oxy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AA; 37232 MW; 4BC3CA090CC556A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                               41; Mismatches 158;
   Pred. No. 3.2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRODG62; IPNSYNTHASE.
PROSITE; PSOD185; IPNS 1, 1,
PROSITE; PSOD186; IPNS 2, 1
SEQUENCE 329 AA; 37232; MW
24.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sopenicillin N synthase.
                               85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces fimbriatus.
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SUCENCE FROW N.A.

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RAMADISTO FROM THE S.E. I. Holt R.A., Hoskins R.A., Galle R.F.,

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RAMADISTO FROM THE S.E., Halt G., Champe M., Heafeffer B.D.,

RAMADISTO FROM R.C., ROGERS Y.-H.C., Bardy R.G., Champe M., Piefiffer B.D.,

RAM R.H., Doyle C., Barker B.G., Helt G., Nelson C.R. Miklos G.L.G.,

RAM ADIIJ W.F., Agbayani A., An H.-J., Andrews PEnnikoch C., Baldwin D.,

RAM BAILW R.W., Bard A., Barnan B.P., Bhandari D., Bossley E.M.,

RAM BAILW R.W., Bard D.A., Bavendala U., Brokstein P., Brottler P.,

RAM BOCKOWS D., Bocchan M.R., Bouck J., Brokstein P., Brottler P., Chandra I.,

RAM BAILW C.M., Cawley S., Dalle C., Davn P., Brandari D., Botcher A., Chandra I.,

RAM BAILW R.W., Deals B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RAM Grerry J.M., Cawley S., Dalle C., Ferriaz C., Ferriar S., Pleischmann W.,

RAM Goden K.J., E. Downes M., Dugan-Rocha S., Dunkov B.C.,

RAM Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAM Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAM Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RAM Lasko P., Lei Y., Leviteky A.A., Li J., Wei M., Nelson D.L.,

RAM Harris N., Watchi B., McIncoh T.C., McLeod M.P., McDerson D.L.,

RAM Mount S.M., May M., Murphy B., Murphy L., Muzny D.M., Nalson H.,

RAM BRID D.R., Nelson K.A., Nixon K., Nusskern D.R., Parla R., Panderson D.L.,

RAM BRID D.R., Nelson K.A., Nixon K., Nusskern D.R., Pand B.,

RAM BRID D.R., Nelson K.A., Nixon K., Nusskern D.R., Wang S., Yao Q.A.,

RAM BRID S.M., Woodege T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RAM BRID S.M., Woodege T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RAM RAM S.M., Woodege T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

RAM RAM S.M., Woodege T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

RAM R.M., Woodege T., 
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A Banzon J., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Feritera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIntosh T.C., Moy W., Murphy S., Patel S., Feiffer B.,
Pacleb J., Paragas V., Park S., Patel S., Feiffer B.,
A Stapleton M., Strong R., Syirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
L. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE PROM N.A.
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                     Last sequence update)
Last annotation update)
   Created)
(TrEMBLrel.
                                     (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                CG5346 protein.
   152 ----FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQA 206
                                                                                                                           176 PEDDILSAVSLIRYPHLKAYPPVKTGPDGTKLSFEDHLDVSVITVLFQTEVQN----LQV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 GF----TGLESESTAQITNTGSYSDYSMCYSMGT---ADNLFPS----GDFGRIWTQYFD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 GYYMAVKGKKAVESWCYLNPSFSEDHPMIRS-GTPMHEVNIWÞDEKRHARFRPFCEQÝYR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 RQYTASRAVAREVLRATGTEPDGGVEA-----FLDCEPLLRFRYFPQVPEHRSAEE-QP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 LSFEDHLDVSMITVLFQTEVQN----LQVETVDGWQDLPTSGENFLVNCGTYMGYLTNDY 247
   17 IRSGTPMHEVNIWPDEKRHERFRPFCEQYYRDMFQLSKTLMRGFALALG-KPEDFFDANL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | | | : | : | : | : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | | | : | | : | | | : | | : | | | : | | | : | | : | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                         207 EVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                                                                                                             232 ETVNGWODLPTSGDDFLVNCGTYMGYLTNDYFPAPNHRV-----KFINAERLSLPFFL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palaniappan N., Seki T.;
"Phylogenetic relationship between the Isopenicillin N synthase (IPNS) and 16S rDNA genes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046951; BAB13299.1; -.
HSSP; P05326; 18K0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces panayensis.
Bacteria, Actinobacteridae; Actinomycetales;
Streptomycineae, Streptomycetaceae; Streptomyces.
NCBI_TaxID=132470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 159; DB 2; Length 262; 25.4%; Pred. No. 1.4e-06; ive 38; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 AA; 30074 MW; D9A5D0BAB942D776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
18openiallin N synthase (IPNS) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002283; IPN synth.
InterPro; IPR002057; ISOpen N synth.
Pfam; PF03171; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00186; IPNS_1; I.
PROSITE; PS00186; IPNS_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 FPAPNHRV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Q9VCZ2;
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Length 403;

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124 INAQNLPEEPLPG-----FADHISTLATDFKALASFILQALAVSLDIPHTFFLEKHSHM 177
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                                                                                                                                                                                                                                                                                                                                             106 --ADNL----FPSGDFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFL----- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 LSGDHDNMSSLRMLYYPPIVDDEPGQNDVIKGRCQYSYQRCLSNQPDFRPEHNPRDEDDL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPY 217
                                                                                                                                                                                                               Palaniappan N., Seki T.;
"Phylogenetic relationship between the Isopenicillin N synthase (IPNS)
                                                                                                                                                                                         3 TTVPTFSLAELQQGLHQ------DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLV
                                                                                                                                                                                                                                                                  52 IDPFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITN-----TGSYSDYSMCYSMGT
                                                                                                                                                                                                                                                                                                      ------VNLP-PDIRQHYIRADGDKHGYVSRGQQQRFDGKSPELRHAFNIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 RPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 LPGSILVNCGEILNIWTQGRYPALQHRVIIPEQETIRARGRHSIAFFCHPDNITTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and 165 TDN genes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB045853 BAB13301.1;
HSSP; P05326; HSKO.
InterPro; IPR002123; 2GG-FeII Oxy.
InterPro; IPR002057; ISOPen N synth.
Pfam; PF03171; 2GG-FeII Oxy.
InterPro; IPR002151; ISOPen N synth.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00186; IPNS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 262;
EMBL; AY102699; AAM27528.1; -.
Flydase; FBgn0038981; CG5346.
Interpro; IPR005123; 2OG-FeII Oxy.
Pfam; PF03171; 2OG-FeII Oxy; 1.
SEQUENCE 403 AA; 45461 MW; DEZCBC0FD443A07C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AA; 30122 MW; 3AFED20F3DB41E69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
150penicillin N synthase (IPNS) (Fragment).
                                                                                                            Query Match 9.6%; Score 156.5; DB 5; Best Local Similarity 20.2%; Pred. No. 4.3e-06; Matches 72; Conservative 51; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI TaxID=132471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 9.5%; Score 156; DB 2; L Local Similarity 25.0%; Pred. No. 2.6e-06; les 62; Conservative 38; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        154 ----DCEPLLRFRYFPQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces heteromorphus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                        76 DDF
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SEQUENCE
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Q9FAC0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 IDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITN-----TGSYSDYSMCYSMGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ADNL----PPSGDFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFL----- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 LSGDHÖNMSSLRMLYYPPIVDDEPGQNDVIKGRCQYSYQRCLSNQPDFRPEHNPRDEDDL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------RMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 LPGSILVNCGEILNIWTQGRYPALQHRVIIPEQETIRARGRHSIAFFCHPDNITTIS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUVPIIDLAHC--GIEEVPVKSVVNRVGHQLKKALSEKGMALLVNHGISDEKLKTAMDHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 DDP-----VNLP-PDIRQHYIRADGDKHGYVSRGQQQRFDGKSPELRHAFNIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TTVPTFSLAELQQGLHQ------DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 RPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFS
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Calamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richer J., Russo S., Searle S.W.J., Smith E., Shu S., Smutniak P., Whitfield E., Shu S., Smutniak P., Whitfield E., "Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    9.6%; Score 156.5; DB 5; Length 403;
20.2%; Pred. No. 4.3e-06;
Live 51; Mismatches 127; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                          Flybase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003139; AAF56013.2;
Flybase; FR200318981; CG5346.
InterPro; IPR005123; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy.
SEQUENCE 403 AA; 45431 MW; DE2CA70E6443A07C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 20.23
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338 YRTYNHGEYSRHYVTSR 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 PAPNHRV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 AA;
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Q9FAB6;
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Matches
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                                                                                                   63 KRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGT-----ADNLFPS--GD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 EKYPMEP-----GGIQGYGHAFVFSDDQKLDWCNMLALGVEPAFIRRPNLWPTTPAN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 GGQVKAPRHH-VAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETAT 293
                                                                    76 GF----TGLESESTAQITNTGSYSDYSMCYSMGT---ADNLFPSGD----FGRIWTQYFD 124
                                                                                                                                                              125 RQYTASRAVAREVLRATGTEPDGGVEA-----FLDCEPLLRFRYFPQVPEHRSAEE-QP 177
                                                                                                                                                                                                                                                      178 LEMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
                                                                                                                                                                                                                                                                              64 IPVIDVGELÖRGSEDELDNLRLACEQWGFFQVVNHGVEEETMEEMEKAARBFFMLPLEEK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 FSKTLEKYSVEIRELCVRLLEHIAAALGLAPARLNGMFGEAVQAVRMNFYPPCPR----P 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
5 VPTFSLAELQQGLHQ--DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

9.4%; Score 154.5; DB 10; Length 366;
Best Local Similarity 22.1%; Pred. No. 5.8e-06;
Matches 70; Conservative 52; Mismatches 158; Indels 37;
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Sasaki T., Mateumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0492699.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003266; BAB64195.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR005123; 20G-FeII Oxy.
PF03171; 20G-FeII Oxy; I.
4CE 366 AA; 40738 MW; 6EC44508E618458E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              238 VKAPRHHV 245
                                                                                                                                                                                                                                                                                                                                                                                        248 FPAPNHRV 255
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094270
070427
AC 09427
AC 09427
DT 01-DE
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DT 01-DE
DT 01-DE
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134 MFRLSKALMRGFALALG-KPEDFFDAPLSEADTLSAVSLIRYPYLEDYPVKTGPDGTKL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GF----TGLESESTAQITNTGSYSDYSMCYSMGTAD--NLFPSGD----FGRIWTQYFDR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 GYYMAVKĞKKAVESWCYLNPSFTEDHPMIRSGAPLHEVNIWPDEKRHERFRPFCEQYYRD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 OYTASRAVAREVLRATGTEPDGGVEA-----FLDCEPLLRFRYFPQVPEHRSAEE-QPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                              Palaniappan N., Seki T.,
"Phylogenetic relationship between the Isopenicillin N synthase (IPNS) and 16S rDNA genes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB045852; BAB13300.1; --
HSSP; PO5326; 1BK0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 RMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces argenteolus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                             Streptomyces hygroscopicus subsp. hygroscopicus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=68042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30112 MW; 449522395CF30653 CRC64;
                                                                                          D1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
D1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Isopenicillin N synthase (IPNS) (Fragment).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.4%; Score 154; DB 2;
262 AA
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InterPro; IPR005283; IPN_synth.
InterPro; IPR002057; ISopen N synth.
Pfan; PF03171; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNSTNTHASE.
PROSITE; PS00185; IPNS_1; 1.
PROSITE; PS00186; IPNS_2; 1.
                                                            Created)
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PRT;
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                                                         01-MAR-2001 (TrEMBLrel, 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 24.7%
nes 61; Conservative
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PRELIMINARY;
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Created)
      PS00185, IPNS_1; 1.
PS00186, IPNS_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 VKAPRHHV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 FPAPNHRV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                               PROSITE; IN NON TER NON TER SEQUENCE
   PROSITE;
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                                                                                                                                                                                                          Query Match
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      STTRB
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                                                                                                                   The Palaniappan N., Seki T.,

Thylogenetic relationship between the Isopenicillin N synthase (IPNS)

Thylogenetic relationship between the Isopenicillin N synthase (IPNS)

Thylogenetic relationship between the Isopenicillin N synthase

Thylogenetic relationship between the Isopenicillin N synthase

Thylogenetic relationship between the Isopenicillin N synthase

Thylogenetic relationship to the EMBL/GenBank/DDBJ databases.

Thylogenetic relationship to the EMBL/GenBank databases.

Thylogenetic relationship 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFTGLESESTAQITNTGSYSDYSMCY-----SMGT---ADNLFPSGD----FG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GY-----YMAVKGRKAVESFCYLNPLFNDEHPMIKSGTPMHEVNIWPDEDRHPGFR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 RIWTQYFDRQYTASRAVAREVLRATGT----EPDGGVEAFLDCEPLLRFRYFPQVPEHR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 TGPDGTKLSPEDHLDVSMITVLFQTQVQN----LQVETVDGWQDLPTSEDNFLVNCGTYM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : | | | : | : | : | : | CINKACKGSGFFYASHGI---DVQRLQDVVNEFHRTMSDQEKYDLAINAYNENNPHVRN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palaniappan N., Seki T.;
Palaniappan N., Seki T.;
Palaniappan N., Seki T.;
Palaniappan N., Seki T.;
Phalaniappan N., Seki T.;
Phalaniappan N., Seki T.;
and 16S rDNA genes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB045865, BAB13298.1;
INTERTO, IPRO05123; 20G-FeII Oxy.
InterPro; IPRO02583; IPN synth.
InterPro; IPRO02057; Isopen N synth.
Pfam; PF03171; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy.
Pfam; PR03171; 20G-FeII Oxy.
Pfam; PR03171; 20G-FeII Oxy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 BFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces viridochromogenes.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.4%; Score 154; DB 2; Length 262;
llarity 24.3%; Pred. No. 4e-06;
Conservative 32; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29991 MW; CFAA44E6D7D307B6 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Isopenicillin N synthase (IPNS) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLVTGGQVKAPRHHV 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 2
262 AA;
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nes 62; Conserv
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                                                                  SEQUENCE FROM N.A.
   WCBI_TaxID=67274;
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SEQUENCE
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92 GFFLVVNHGVDDKLIAHAHQYIDYFFELPMSAKQRA-----QRKVGEHCGYASSFTGR 144
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                                                                                                                                                                                                                                                                                                                                                                                               76 GF----TGLESESTAQITNTGSYSDYSMCYSMGT---ADNLFPSGD----FGRIWTQYFD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 RQYTASRAVAREVLRATGTEPDGGVEAFL---DCEPLLRFRYFPQVPEHRSAEEQP---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 LSFQDHLDVSMITVLFQTEVQN----LQVETVDGWQDLPTSGDHFLVNCGTFMGYLTNDY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 SRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFP--QVPEHRSAEEQPLRMAPHYDLS 187
                                                                                                                                                                                                                                                                                          21 BFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK----RAVTSPVPTMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fagus sylvatica (Beechnut).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fagales; Fagaceae; Fagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRR-----GFTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calvo A., Lorenzo O., Nicolas C., Rodriguez D., Nicolas G.; "Molecular cloning and transcript analysis of a functional GA20 oxidase related to the release from dormancy in Fagus sylvatica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.3%; Score 152; DB 10; Length 379;
Best Local Similarity 24.3%; Pred. No. 1e-05;
Matches 67; Conservative 40; Mismatches 105; Indels 6
                                                                                                     Length 262;
                                                                                                         Query Match 9.3%; Score 152; DB 2; Length 26
Best Local Similarity 25.0%; Pred. No. 6.2e-06;
Matches 62; Conservative 39; Mismatches 115; Indels
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InterPro; IPR05123; 2OG-FeII OXY.
InterPro; IPR05223; IPN_Bynth.
Pfam; PF01171; 2OG-FeII OXY; 1.
PRINTS; PR0682; IPNSYNTHARS.
SEQUENCE 379 AA, 43056 MW; E3E51A2FC94EFBB3 CRC64;
262 262
262 AA; 30107 MW; D72BF9737CC8EAEB CRC64;
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Last annotation update)
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240		S 301
GQVKA	<u></u>	GRYKS
TLVTG	::	MALSN
AVLVFCGAIATLVTGGQVKA 240		'GGLQVFVDEEWRSITPNFNAFVVNIGDTFMAI
VLVF		Ž
-DA		FNA
AFTDLPYRP		SITPN
LPYR	••	EEWR
AFTDI	_	VEVD
AEVGGA	=	GGLQ
AEV		õ
VSLC		į
TLIQQTPCANGFVSLQ		
TPC	_	5
MVTLIQO	::	TILH
≥		253 SLT
188		253

²⁴¹ PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVP 276
302 CLHRAVVNSK----TPRKSLAFFLCPKNDKVVSPP 332

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Search completed: February 3, 2004, 17:38:34 Job time : 44 secs

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PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
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Sequence 8, A
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Sequence 17,
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(c) 1993 - 2004 Compugen Ltd.
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US-09-13-211-18 Sequence 18, Application US/09413231 Patent No. 6284483 GENERAL INFORMATION GENERAL INFORMATION APPLICANT: Radyrzhanova, Dina K APPLICANT: Mandy Zhenyong TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate TITLE OF INVENTION WHORE: US/09/413,231 CURRENT FILING DATE: 1999-10-06 SEQ ID NOS: 18 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NOS: 18 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NOS: 18 SOFTWARE: PRT TYPE: PRT CORGANISM: Artificial Sequence FRATURE: FRATURE: FRATURE: CONTER INFORMATION: from Streptomyces clavuligerus NAME/KEY: WUTAGEN OTHER INFORMATION: Ala181 in native DAOCS modified to Arg UCCATION: (181) COTHER INFORMATION: Ala181 in native DAOCS modified to Arg US-09-413-231-18 GUETY MATCH BEST LOCAL SIMILATITY 99.4%; Pred. NO. 2.3e-176; MATCHES 309; Conservative 0; Mismatches 2; Indels 0; Gaps 0; MATCHES 309; CONSERVATION: (181)	3 89 5.4 377 3 US-08-784-385-4 Sequence 4, 4 84.5 5.2 430 4 US-09-252-991A-22599 Sequence 225 5 84 5.1 218 4 US-09-252-991A-26105 Sequence 26	210000700	108.5 6.6 390 4 US-09-252-991A-20513 Sequence 205 106 6.5 241 2 US-08-379-556A-4 Sequence 4, 2 US-08-379-556A-4 Sequence 4, 37 3 US-09-413-231-6 Sequence 6, 377 5 PCT-US95-10403-4 Sequence 6, 36 5.9 357 4 US-09-645-168-3 Sequence 3, 36 5.9 412 3 US-09-072-064-4 Sequence 3, 395.5 5.9 412 3 US-09-072-064-4
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                            Sequence 15, Application US/08592411
Patent No. 572603
GENERAL INFORMATION:
TITLE OF INVENTION: 7-ADCA via 2-(Carrier OF INVENTION: 3-(Carboxymethyl)
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/592,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 17, Application US/08592411; Patent No. 5726032; GENERAL INFORMATION: TITLE OF INVENTION: 7-ADCA via 2-((;); TITLE OF INVENTION: 7-ADCA via 2-((;); TITLE OF INVENTION: 3-(Carboxymeth); NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 70.39
Matches 218; Conservative
                                   301 NYVNIRRTSKA 311
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YINIRKTAAA 312
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US-08-592-411-15
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT SPETICATION SPETICATION DATA:
APPLICATION NUMBER: US/08/592,411
FILING DATE:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 anino acids
TYPE: amino acid
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APPLICANT: Coque, Juan R.
APPLICANT: Coque, Juan R.
APPLICANT: Brightia, Francisco J.
APPLICANT: Functe, Juan L.
APPLICANT: Liarena, Francisco J.
APPLICANT: Liras, Paloma
APPLICANT: Liras, Paloma
TITLE OF INVENTION: DNA ENCODING CEPHAMYCIN BIOSYNTHESIS
TITLE OF INVENTION: LATE GENES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                                                                                                                           72.5%; Score 1186.5; DB 1
69.8%; Pred. No. 1.5e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-04801-6; Sequence 6, Application PC/TUS9504801; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.8*
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 NYVNIRRISKA 311
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                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-592-411-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rahway
STATE: New Jersey
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10.0%; Score 164; DB 3; Length 32; 23.8%; Pred. No. 4.2e-10; cive 50; Mismatches 150; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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ORGANISM: Artificial Sequence
FEATURE:
                                                        Query Match
Best Local Similarity 23.8%
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION:
NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
LENGTH: 329
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US-09-413-231-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 EKQAVTTKVPTWRRGYSALEAESTAQVTNTGTYTDYSMSYSMGIGGNLPPSKEFESVWTD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DKTVPVFSMAELRDGSRODEFREWAR-RGVFYLTGYGATERDHRVATDTAMDFFAQGTAE 61
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Patent No. 6284483

Patent No. 6284483

GENERAL INFORMATION:

APPLICANT: Dilley, David R

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate

FILE REPRENCE: MSU41-453

CURRENT APPLICATION NUMBER: US/09/413,231

CURRENT FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 310;
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OTHER INFORMATION: Glu210 in native IPNS modified to Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.0%; Score 965.5; DB 5; Best Local Similarity 61.2%; Pred. No. 2.1e-101; Matches 186; Conservative 37; Mismatches 80;
                                                                        ALIONED FACE AND THE A
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ORGANISM: Artificial Sequence
                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein PCT-US95-04801-6
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US-09-413-231-5
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                                                                                                                                                                                                                                                                         59 SEAEK----RAVTSPVPTMRRGF----TGLESESTAQITNTGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                          107 DNLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVBA-----FLDCE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 VNLWPDEERHPRFRPFCEGYYROMLKLSTVLMRGLALALG-RPEHFFDAALAEQDSLSSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 PTSENDFLVNCGTYMAHVTNDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
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                                                                                                                                                                              10 VPIDISPLFGTDAAAKKRVAEEIHGACRGSGFFYATNHGV---DVQQLQDVVNEFHGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL
                                                                                                                                    5 VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
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Best Local Similarity 23.8%; Pred. No. 4.2e-10;
Matches 77; Conservative 50; Mismatches 150; Indels 46; Gaps
                                                                         46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09413231
| Patent No. 6284483
| GENERAL INFORMATION:
| APPLICANT: Dilley, David R
| APPLICANT: Warner, Toni M
| APPLICANT: Warner, Toni M
| TITLE OF INVENTION: Medified Synthetases To Produce Penicillins and TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate FILE REFERENCE: MSU41-453
| CURRENT APPLICATION NUMBER: US/09/413,231
| CURRENT FILING DATE: 1999-10-06
| NUMBER OF SEQ ID NOS: 18
Length 329;
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us-09-582-486-1.rai

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223 LVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECG 282
                                                                                                                        55 FEHGSEAEKRAVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 BAPLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVG 209
163 YFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAV 222
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                                            205 YYPPCP----CPELALGVAPHTDMSSITIL----VPNEVQGLQVFKDGQWYDVAYIPNAL
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                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: HOLTON, TIMOTHY A.

APPLICANT: HOLTON, TIMOTHY A.

APPLICANT: HOLTON, TISA A.

TITLE OF INVENTION: SYNTHASE ENZYMES AND USES THEREFORE NUMBER OF SEQUENCES: 2.1

CORRESPONDENCES: 2.1

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,556A FILING DATE: 22-MAR-1995 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: DIGGLIO, FRANK 31,346 REGISTRATION NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 9592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08379556A
Patent No. 5859329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (516)742-4346
TELEFAX: (516)742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        283 FDVSLDGETATFQDWI 298
                                                                                                                                                                                                                                       311 KDDPPKYKTKKYKDYV 326
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amino acid
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                                                                                                                                                                                                                                                                                                                                  US-08-379-556A-8
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126 VNLWPDEERHPRFRPFCEGYYRQMLKLSTVLMRGLALALG-RPEHFFDAALAEQDSLSSV 184
                                              157 PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
                                                                                          185 SLIRYPYLEEYPPVKTGPDGQLLSFRDHLDVSMITVLFQTQVQN----LQVETVDGWRDI 240
                                                                                                                                       PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV 275
                                                                                                                                                                                     241 PISENDFLVNCGIYMAHVINDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 VIAKP-----DGYKGVE-----GYGTKLQKEVQGKKGWVDHLFHIVWPPSFINYQFW 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 TQ----YFD--RQYTASR-AVAREVL----RATGTEPD-----GGVEAFLDCEPLLRFR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKR
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9.9%; Score 162; DB 2; Length 335;
Best Local Similarity 22.8%; Pred. No. 7.3e-10;
Matches 72; Conservative 55; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08379556A
Patent No. 5859329
GENERAL INFORMATION:
APPLICANT: HOLTON, TIMOTHY A.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOL
TITLE OF INVENTION: SENTHASE ENZYMES AND USES THEREFORE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSERS
SCHLLY SCOTT MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: BATCHIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/379,556A
FILING DATE: 22-MAR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S.
                                                                                                                                                                                                                                       276 PLARECGFDVSLDGETATFQDWI 298
                                                                                                                                                                                                                                                                  294 PFVPE-GASEEVRNEALSYGDYL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9592
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4346
TELEFAX: (516)742-4366
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 335 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: GARDEN CITY STATE: NEW YORK
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US-08-379-556A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                         216
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242 GRWYDVKYIPNALLIHVGDQMEIMSNGEYKAVLHRSTVNKE----RTRISWPVFLEPPS 296

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66 MTDQEKHDLAIHAYNENNSHVRNGY------YMARPGRKTVESWCYLNPSFGEDHPM 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GSEAEK-----RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCY---SMGTADNL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 FPSG-----EPDGTIWTQYFDRQYTASRA-VAREVLRATGT-----EPDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 IKAĞTPMHEVNVWPDEERHPDFRSFGEQYYREVFRLSKVLLLRĞFALALĞKPEEFFENEV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 LOAEVGGAFTDLPYRPDAVLVFCGALATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 LOVETVDGWQSLPTSGENFLINCGTYLGYLTNDYPPAPNHRV-----KYYNAERLSLPF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 VPTIDISPL-FGTDPDAKAHVARQINEACRGSGFFYASHHGI---DVRRLQDVVNEFHRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VPTFSLAELQQGLHQD-----EPRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GVEAFLDCEPL-LRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from streptomyces anulatus (S. lipmanii) NAME/KEY: MUTAGEN
                                                                                   APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REPERENCE: MSU41-453
CURRENT APPLICATION NUMBER: US/09/413,231
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PLENTING Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.7%; Score 143; DB 3; Length 333; Best Local Similarity 23.2%; Pred. No. 1.1e-07; Matches 70; Conservative 37; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (214)
OTHER INFORMATION: Glu214 in native IPNS modified to Arg
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US-08-379-556A-2
; Sequence 2, Application US/08379556A
; Detent No. 5859329
; GENERAL INFORMATION:
                  Sequence 10, Application US/09413231
Patent No. 6284483
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-413-231-10
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85 TAQITNTGSYSDYSMCYSMGTADNLF----PSGDFGRIW-------TQYFDRQYT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 ASRAVAREVLRATGTEPDGGVEAFLDCE--PLLRFRYFPQVPEHRSAEEQPLRMAPHYDL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 VVDRIFKSLSLGLGLEGHEMIEAAGGDEIVYLLKINYYPPCPR----PDLALGVVAHTDM 237
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Parent No. 6284483

GENERAL INFORMATION:
APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Warner, Toni M
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 347;
        APPLICANT: KEAM, LISTA A.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOL
TITLE OF INVENTION: SYNTHASE ENZYMES AND USES THEREFORE
TORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULX SCOTT MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                              COMPUTER RELABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,556A
FILING DATE: 22-MAR-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.6%; Score 140; DB 2;
Best Local Similarity 22.3%; Pred. No. 2.5e-07;
Matches 59; Conservative 43; Mismatches 114
                                                                                                                                                  ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 APRRDQIAGSSRTSSVFFLRPNAD 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9592
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4366
APPLICANT: HOLTON, TIMOTHY A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                      11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 EVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 GSEAEKRAVISPVPIMRRGFIGLESESTAQ----IINIGSYSDYSMCY---SMGTADNLF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ----ESTTWTDQRSTTWRSTRYNENNSHVRNGYYMARPGRETVESWCYLNPSFGEDHPMM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 PSG-----AREVLRATGEPDGGV-- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 KAĞIPMHEVNVWPDEERHPDFGSFGEQY-HREVSASRRCCCGASRWRRQAGESSSNEVTE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 EAFLDCEPLLRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 ETVDGWQSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPFFLH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VPTFSLABLOQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VPTIDISPQLFGTDPTPRATSRGRSTRPARGSGFFYASHHGIDVRRLQTWSN-----
                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from Streptomyces cattleya NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from Penicillium chrysogenum NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MSU41-453
CURRENT APPLICATION NUMBER: US/09/413,231
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.4%; Score 137; DB 3; Length 321; Best Local Similarity 23.1%; Pred. No. 4.8e-07; Matches 73; Conservative 32; Mismatches 149; Indels
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COTHER INFORMATION: Glu212 in native IPNS modified to Arg
US-09-413-231-4
                                                                                                                                                                                                                                                                                                                   ; LOCATION: (211); OTHER INFORMATION: Glu211 in native IPNS modified to Arg US-09-413-231-8
                 CURRENT APPLICATION NUMBER: US/09/413,231
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 8
LENGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09413231; Patent No. 6284483; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 AGQNSVMK-PFTRRTG 301
                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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FILE REFERENCE: MSU41-453
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US-09-413-231-4
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LENGTH: 331
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197 PAAIKTAEDGTKLSFRWHEDVSLITVLYQSDVAN----LQVEMPQGXLDIEADDNAYLVN 252
                                                                                                                                                                                                                                                                                                                                                                      137 GFREFABÓYYWDVFGLSSÁLLKGYALÁCKBEDFFSRHFKKEDALSSVVLÍRYPÝLNPIÞ 196
                                                                                                                                                                                                                                                                                                                                                                                                                               169 EH--RSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 CGSYMAHITINNYYPAPIHRV-----KWVNEERQSLPFFV--NLGFNDTVQPWDPSKEDG 304
                                                                                                                                                                                                                  61 -AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTAD--NLFPS----G 113
                                                                                                                                                                                                                                                                 94 IPEKKAVES-----FCYL-----NPNFKPDHPLIQSKTPTHEVNVWPDEKKHP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDV 285
                                                                                                                                                           37 RDTGFFYAVNHGVDVKRLSNKTREFHFSITDEE---KWDLAIRAYNKEHQDQIRAGYYLS 93
                                                                                                                                                                                                                                                                                                                          114 DFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAF-----LDCEPLLRFRYFPQVP
                                                                                                          27 RDKGLFYLTDCG------LTDTELKSAKDLVIDFF--EHGSE----
                                                      Gaps
                                                   73;
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APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEGUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
     Length 331;
  8.2%; Score 133.5; DB 3; Length 324.1%; Pred. No. 1.3e-06; tive 39; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., Suite 800
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N: 800
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,367A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49/FD4.5MZ
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REGISTRATION NUMBER: 40,949
REFLECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
TELEFAX: 202-721-8250
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SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
Query Match
Best Local Similarity 24.18
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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20006
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MOLECULE TYPE:
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                                                                                                                 CLONE:
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                                                                                                                                                                                                                                    ----TAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVLRA 140
                                                                                                                                                                                                                                                                                                                                                               TGTEPDGGVEAFLDCEPLLRFRYFP--QVPEHRSABEQPLRMAPHYDLSMVTLIQQTPCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                             199 NGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 NG---LQVFVDNQWQSIRPNPKAFVVNIGDTFWALSNGIFKSCLHRAVVNRE-----SAR 311
                                                                                                                                                                                                            30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPT--MRRGFTGLESES---
                                                                                                                                                                      28;
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Sequence Application US/09295306
Patent No. 6198021
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
                                                                                                                                 8.0%; Score 131; DB 2; Length 378; llarity 23.3%; Pred. No. 3e-06; Conservative 40; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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TEPERENCE/POCKET NUMBER: 49/DIV-FD4.5MZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/53,367
FILING DATE: NO. 6198021ember 27, 1995
ATTORNEY/AGENT INFORWATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: zu pAT2353
US-08-553-367A-6
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/09/
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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D.C.
U.S.A.
                                                                                                                                 Query Match
Best Local Similarity
Matches 60; Conserv
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US-09-295-306-6
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85 ----TAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVLRA 140
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                                                                                                                                                                                                                                                                                                                                                                      30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPT--MRRGFTGLESES---
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TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                  Query Match

8.0%; Score 131; DB 3; Length 378;
Best Local Similarity 23.3%; Pred. No. 3e-06;
Matches 60; Conservative 40; Mismatches 130; Indels
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REPERENCE/DOCKET UNBER: 2000-1678/LC/01784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb.
COMPUTER: IDEM COMPATIBLE
COMPUTER: IDEM COMPATIBLE
COMPATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,719
FILING DATE: 13-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
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APPLICATION NUMBER: 09/295,306
RILING DATE: April 21, 1999
APPLICATION NUMBER: 08/553,367
RILING DATE: NO. 6455675ember 27,
APPLICATION NUMBER: PCT/EP94/01664
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ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                              ORGANISM: Arabidopsis thaliana IMMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09734719
Patent No. 6455675
GENERAL INFORMATION:
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protein
NO
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                          HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
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85 ----TAQITINTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVLRA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 TGTEPDGGVEAFLDCEPLLRFRYFP--QVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 NG---LÖVFVDNQWQSIRPNPKAFVVNIGDTFMALSNGIFKSCLHRAVVNRE----SAR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPT--MRRGFTGLESES--- 84
                                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                         Query Match 8.0%; Score 131; DB 4; Length 378; Best Local Similarity 23.3%; Pred. No. 3e-06; Matches 60; Conservative 40; Mismatches 130; Indels 2
| INFORMATION FOR SEQ ID NO: 6:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 378 amino acids
| TYPE: amino acid |
| TYPE: amino acid |
| STRANDEDNESS: single |
| TYPE: amino acid |
| STRANDEDNESS: single |
| TYPE: protein |
| HYPOTHETICAL: NO |
| AMTI-SENSE: NO |
| ORIGINAL SOURCE: ORGANISM: Arabidopsis thaliana |
| IMMEDIATE SOURCE: |
| CLONE: ZU PAT2353 |
| US-09-734-719-6
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Sequence 18, Appl
Sequence 12239, A
Sequence 5, Appli
Sequence 14043, A
Sequence 10, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 17939, A
Sequence 17939, A
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14020, A
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1 MDTTVPTFSLAELQQGLHQD.....ATFQDWIGGNYVNIRRTSKA 311
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-369-493-12239
US-09-924-841-5
US-10-369-493-14043
US-10-369-493-14043
US-10-136-444-8
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US-10-369-841-8
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 1, Appli
Sequence 3, Appli
Sequence 13, Appli
Sequence 13, Appl
Sequence 1955, A
Sequence 78, Appl
Sequence 1995, A
Sequence 1995, A
Sequence 1394, A
Sequence 13096, A
Sequence 13096, A
Sequence 13, Appli
Sequence 13, Appli
Sequence 6, Appli
Sequence 138, Appli
Sequence 1677, Appli
Sequence 1678, Appli
Sequence 16
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Sequence 124, App
US-10-369-493-19206

US-09-924-841-3

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US-09-924-841-3

US-09-924-841-3

US-10-369-493-13125

US-10-369-493-19952

US-10-369-493-19952

US-10-369-493-19952

US-10-369-493-19952

US-10-369-493-13046

US-10-369-493-13046

US-09-924-841-6

US-09-924-841-6

US-09-924-841-6

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US-09-924-841-7

US-09-924-841-6

US-09-931-305-6

US-09-931-305-6

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ALIGNMENTS

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                               Sequence 18, Application US/09924841

Sequence 18, Application US/09924841

Sequence 18, Application US/09924841

GENERAL INFORMATION:

APPLICANT: Mang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

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TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION WORDER: US/09/413,231

CURRENT PILING DATE: 1999-10-06

PRIOR FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 18

LENGTH: BT

TYPE: PRT

TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified DAOCS
OTHER INFORMATION: from Streptomyces clavuligerus
NAME/KEY: WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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, OTHER INFORMATION: Ala181 in native DAOCS modified to Arg
US-09-924-841-18
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US-09-924-841-18
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US-10-369-493-7649 US-10-369-493-14020 US-10-369-493-12421 US-10-369-493-4891

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Sequence 5, Application US/09924841 Patent No. US20020127633A1
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 10/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
                                                                                                                                                                                181 RPHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLYTGGQVKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 EHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 AL-PEADKLAIEMVKSSQFRGYTRAGGELTK-----GREDWREQLDIGVERQAIAQGPG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 RFRYFPQVPEHR-SAEEQPLR------MAPHYDLSMVTLIQQTPCANGFVSLQAEVGG 210
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61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120
                          61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCTSMGTADNLFPSGDFERIWT 120
                                                                           QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180
                                                                                                    121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYPQVPEHRSAEEQPLRM 180
                                                                                                                                                       181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 240
                                                                                                                                                                                                                                       PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                                                                             241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12239, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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24.7%;
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ORGANISM: Mesorhizobium loti
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US-10-369-493-12239
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59 SEAEK----RAVTSPVPTMRRGF----TGLESESTAQITNTGSYSDYSMCYSMGT---A 106
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GENERAL INFORMATION:
APPLICANT: Dilley, David R
APPLICANT: Radyzanova, Dina K
APPLICANT: Radyzanova, Dina K
APPLICANT: Wang Zhenyong
APPLICANT: Wang Zhenyong
APPLICANT: Wang Zhenyong
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MSU41-453
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5
LENGTH: 329
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FEATURE:
OTHER: INFORMATION: Description of Artificial Sequence: modified IPNS
OTHER INFORMATION: from Streptomyces clavuligerus
NAME/KEX: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09924841
Sequence 9, Application US/09924841
Patent No. US20020127633A1
GENERAL INFORMATION:
APPLICANT: Billey, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate FILE REPERENCE: MOUAL-453
CURRENT APPLICATION NUMBER: US/09/924,841
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CTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-5
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10.0%; Score 164; DB 10;
Best Local Similarity 23.8%; Pred. No. 2.3e-09;
Matches 77; Conservative 50; Mismatches 150;
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58 GSEAEK-----RAVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCY---SMGTADNL 109
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                                                                                                                         60 EAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIW 119
                                                                                                                                                                        60 DSEKNAVGMINSPHFRGYNRAASEITR-----GQPDQREQFDLGAERDVLPLNADSPLW 113
                                                                                                                                                                                                                         120 TQ-----TEPDGGVEAFLDCEPLL 159
                                                                                                                                                                                                                                                                                                                              160 RFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEV-GGAFTDLPYR 218
                                                                                                                                                                                                                                                                                                                                                                            173 HIKLMRYPGQASTASNQ--GVGAHKDSGFLSFLLQDQQA----GLQVEIEEGRWIDALPR 226
                                                                                                                                                                                                                                                                                                                                                                                                                              219 PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD----FTF 273
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                                                        Sequence 10, Application US/09924841
| Patent No. US20020127633A1
| GENERAL INFORMATION:
| APPLICANT: Dilley, David R
| APPLICANT: Wang, Zhenyong
| APPLICANT: Wang, Zhenyong
| APPLICANT: Warner, Toni M
| TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
| TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
| FILE REPERENCE: MSU41-453
| CURRENT APPLICATION NUMBER: US/09/924,841
| CURRENT PILING DATE: 1999-10-06
| PRIOR FILING DATE: 1999-10-06
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                         ---OCCLHODEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
OTHER INFORMATION: from streptomyces anulatus (S. lipmanii)
INCATION: (214)
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 333
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 DNLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEA-----FLDCE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 SEAEK-----RAVISPVPIMRRGF----IGLESESTAQITNTGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 VNLWPDEERHPRFRPFCEGYYRQMLKLSTVLMRGLALALG-RPEHFFDAALAEQDSLSSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 PTSENDFLVNCGTYMAHVTNDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 VPTIDISPLFGTDAAAKKRVAEEIHGACRGSGFFYATNHGV---DVQQLQDVVNEFHGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from Streptomyces clavuligerus strain NRRL 3585 NAMB/KEY: MUTAGEN LOCATION: (210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 164; DB 10; Length 329; 23.8%; Pred. No. 2.3e-09; tive 50; Mismatches 150; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.1%; Score 148.5; DB 12; Length
23.8%; Pred. No. 1.2e-07;
tive 43; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/413,231
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 9
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 PFVPE-GASEEVRNEALSYGDYL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14043, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLARECGFDVSLDGETATFQDWI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 23.84
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Conservative
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Best Local Similarity
Matches 80; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-10-369-493-14043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-10-369-493-14043
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                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 RGFFRLPITAKQQYANLP----RTYEGYGSRVGVQKGGPLDWGDY---YFLHLAPDAGK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 SGDFGRIWTQYFDRQYTASRAVAREVLR------ATGTEPDGGVEAF--LDCEPL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 LRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 HDAFIVNVGDQIQILSNSMYKSVEHRVMVNAKEE----RISLALFYNPRGD----VPIA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8 Application US/09924841

Patent No. US20020127633A1

Patent No. US20020127633A1

GENERAL INFORMATION:

APPLICANT: Dilley, David R

APPLICANT: Wardy Zhenyong

APPLICANT: Wang, Zhenyong

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate

FILE REFERENCE: MG414-83: US/09/924,841

CURRENT APPLICATION NUMBER: US/09/924,841

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LINGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDTTVPTFSLAELQQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLV
                                                                                                                                                                                                                                                                                                                                                                                                   47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from Streptomyces cattleya NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 321;
                                                                                                                                                                                                                                                                                                                                                  Query Match 8.5%; Score 139.5; DB 12; Length Best Local Similarity 23.3%; Pred. No. 1.5e-06; Matches 70; Conservative 43; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to Arg
                    TITLE OF INVENTION: Compositions isolated from forage TITLE OF INVENTION: grasses and methods for their use. FILE PERERRICE: 11000-110659 CURRENT APLICATION NUMBER: US/10/431,273 CURRENT FILING DATE: 2003-05-06 NUMBER OF SEQ ID NOS: 92 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 88 LENGTH: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNS modified
US-09-924-841-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
8.4%; Score 137; DB 10;
Best Local Similarity 23.1%; Pred. No. 2.3e-06;
Matches 73; Conservative 32; Mismatches 149;
Forster, Richard L. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-431-273-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-924-841-8
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Publication No. US2003010147741

GENERAL INFORMATION:

APPLICANT: COLLIVER, Steven P.

APPLICANT: WILE, Shelpen G.

APPLICANT: WILE, Shelpen R.

APPLICANT: TUNEN van, Adrianus J.

APPLICANT: TUNEN van, Adrianus J.

APPLICANT: VERHOEYEN, Martine E.

TITLE OF INVENTION: A PROCESS POR INCREASING THE FLAVONOID CONTENT OF A PLANT AND PLA

TITLE OF INVENTION: DETAINABLE THEREBY

FILE REFERENCE: 056159-5106

CURRENT PEPLICATION NUMBER: US/10/136,444

CURRENT FILING DATE: 2001-08-20

PRIOR FILING DATE: 2001-08-20

PRIOR FILING DATE: 2001-05-02

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ASRAVAREVLRATGTEPDGGVEAFLDCE--PLLRFRYFPQVPEHRSAEEQPLRMAPHYDL 186
177 TEEDTLSCRSLMIRYPYLDPYPEAAIKTGPDGTRLSFRDHLDVSMITVLPQTBVQN---- 232
                                                                            LQAEVGGAFTDLPYRPDAVLVFCGALATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                          233 LQVETVDGWQSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --TQYFDRQYT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 EGK------KĠWVDHLFHKIWPPSAVNYRYWPKNPPSYREANEEYGKKMRE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 VVDRIFKSLSLGLGLGLEGHEMIEAAGGDEIVYLLKINYYPPCPR----PDLALGVVAHTDM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 SMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 SYITIL----VPNEVQGLQVFKDGHWYDVKYIPNALIVHIGDQVEILSNGKYKSVYHRTT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%; Score 140; DB 15; Length 359; 22.3%; Pred. No. 1.2e-06; tive 43; Mismatches 114; Indels 4
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APPLICANT: Shenk, Michael Andrew
APPLICANT: Glenn, Matthew
APPLICANT: Golonn, Matthew
APPLICANT: Saulsbury, Keith Martin
APPLICANT: Hall, Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 TAQITNTGSYSDYSMCYSMGTADNLF----PSGDFGRIW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 APRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 VNK-----DKTRMSWPVFLEPPSE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 88, Application US/10431273
Publication No. US20030237108A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Petunia hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                             FL 265
                                                                                                                                                                                                                           287 FL 288
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US-10-431-273-89
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                                                                                                                                                                             264
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                                                                            204
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APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLB OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 IPEKKAVES------FCYL-----NPNFKPDHPLIQSKTPTHEVNVWPDEKKHP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 -AEKRAVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCYSMGTAD--NLFPS----G 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 GFREFAEQYYWDVFGLSSALLRGYALALGKEEDPFSRHFKKEDALSSVVLIRYPYLNPIP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 EH--RSAEB-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 PAAIKTAEDGTKLSFRWHEDVSLITVLYQSDVAN----LOVEMPQGYLDIEADDNAYLVN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 CGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 CGSYMAHITHNYYPAPIHRV-----KWVNEEROSLPFFV--NLGFNDTVQPWDPSKEDG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                  Sequence 4, Application US/09924841

Patent No. US20020127633A1

GENERAL INCRNATION:

APPLICANT: Wand:

APPLICANT: Wadyrzhanova, Dina K

APPLICANT: Warner, Toni M

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: MODIFIED SOUTH APPLICATION NUMBER: US/09/924,841

CURRENT APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

SEQ ID NO 4

LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 RDTGFFYAVNHGVDVKRLSNKTREFHFSITDEE---KWDLAIRAYNKEHODQIRAGYYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 DFGRIWTOYFDROYTASRAVAREVLRATGTEPDGGVEAF----LDCEPLLRFRYFPQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 RDKGLFYLTDCG------LTDTELKSAKDLVIDFF--EHGSE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
OTHER INFORMATION: from Penicillium chrysogenum
LOCATION: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.2%; Score 133.5; DB 10; Length 331;
Best Local Similarity 24.1%; Pred. No. 5.8e-06;
Matches 77; Conservative 39; Mismatches 131; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Glu212 in native IPNS modified to Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7649, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 SLDGETATFQDWIGGNYVNI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 KTDQRPISYGDYLQNGLVSL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-369-493-7649
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLB OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT PILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17939
                                                                                                                                                                                                                                                                                                                                                                                  177 EDTLSAVSMIRYPYLDPYPEAAIKTGPDGTRLSFRDHLDVSMITVLSKTEVQN----LQV 232
                                                                                                                                                                                                                                                                  EVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | : | : | : | | | | | ETVDGWQSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPFFLH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 KGATHVDLKEFWHIGRQLAAGHRFADVMAPNIWPTRPEG--FRETFIELFAAFDAAGDKL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRAT----GTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 QTPCANGFVSLQAEVGG-AFTD----LPYRP--DAVLVFCGAIATLVTGGQVKAPRHHY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQ----ITNTGSYSDYSMCY---SMGTADNLF 110
                                                                                                                                                    --DEGRIWTQYFDRQYTASRAV---AREVLRATGTEPDGGV-- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 NTGSYSDYSMCYSMG-----TADNLFPSGDFGRIWTQYFDRQYTASRAVAREV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPTFSLAELQQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH 57
                                                                                                                                                                                                                                                                                                                                              EAFLDCEPLLRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                   10 VPTIDISPQLFGTDPTPRRTSRGRSTRPARGSGFFYASHHGIDVRRLQTWSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 VNPPAER-RGHSRYSMPPFLHPAPDF 253
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 PNADFTFSVPLARECG 282
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Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: SPHINGOMONAS
US-10-369-493-17939
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US-10-369-493-17939
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFREENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLIING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT OF THE CANADA CONTRACT ON THE CANADA CONTRACT OF THE CANADA CONTRACT 
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                                                                                                                                                                        123 FDRQYTASRAVAREVLR----ATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPL 178
                                                                                                                                                                                                                                               194 GAGAHTDYGCITLLYQ-DAAGG---LQVKNVKGQMIDAPPIDGTFVVNLGDMMARWSNDR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 YTA----SRAVAREVLRATGTE---PDGGV-----EAFLDCEPLLRFRYFPQVPEHRS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 ITAFCNYLTQSVNRRLLTLFSRVLELPDDYLWENVQSHGFPTGEGYFRHALFRPVQKETQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 LRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVP-----TMRRGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 VKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 YRSTPHRVISP----LGVDRYSMPFFAEPHPD 277
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NAME/KEY: unsure

LOCATION: (1)..(331)

OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12421
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Publication No. US20030233675A1
GENERAL INFORMATION:
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82-10-36-93-4891
; Sequence 4891, Application US/10369493
; Publication No. US20030233675A1
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION UNMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FPVETKRRAA---VNHRHRGFNALGDATMYQ----AKRPDYKEFFSIGLE---LPEDDPD 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 HGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGD-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --FGRI-----WTQYFDR----QYTASRAVAREVLRAT----GTEPDGGVEAFLDC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 VLAGQALRGPNNWPDFMPELRPALYGYYEAVGACGADLLRAVAVSLGVEEQFFAPRYTKR 170
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; Pred. No. 1.9e-05;
43; Mismatches 161; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 320;
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7.8%; Score 128; DB 12; Length 32
1 Similarity 22.7%; Pred. No. 2.3e-05;
62; Conservative 39; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 LESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRI----
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/360,039
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Burkholderia cepacia
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Best Local Similarity 21.6%;
Matches 71; Conservative 4
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14020
LENGTH: 320
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Best Local Similarity
Matches 62; Conserv
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US-10-369-493-14020
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US-10-369-493-14020
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ORGANISM:
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APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-22
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 LLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPY 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 RPDAVLVFCGAIATLVTGGOVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPL 277
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Job time : 34 secs
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                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4891
Cao, Yongwei
Hinkle, Gregory J.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                               7.64
Best Local Similarity 21.53
Matches 70; Conservative
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Sequence 32088, A Sequence 11094, A Sequence 18, Appl Sequence 121286, Sequence 6, Appli Sequence 6, Appli Sequence 10913, A

Sequence 12239, A Sequence 12239, A Sequence 89855, A Sequence 5, Appli Sequence 9, Appli

AAA

Sequence Sequence Sequence

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Sequence 4796, Ap Sequence 89857, A Sequence 9085, Ap Sequence 12239, A

Sequence 10914, A Sequence 4795, Ap Sequence 94436, A

us-09-582-486-1 rapm

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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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APPLICANT: ILOYD, Matthew D.
APPLICANT: LOYD, Matthew D.
APPLICANT: HARLOS, Karl
APPLICANT: ANDERSONO, Inger
APPLICANT: ANDERSONO, Inger
APPLICANT: TERMISSCHA VAN SCHELTINGA, Anke S.
APPLICANT: RAMASWAMY, S.
APPLICANT: RAMASWAMY, S.
APPLICANT: RAMASWAMY, S.
TITLE OF INVENTION: X-RAY STRUCTURE
FILE REPERBENCE: 08004624
CURRENT PILING DATE: 2000-06-23
FRICA FILING DATE: 1997-12-24
FRICA FILING DATE: 1997-12-24
FRICA FILING DATE: 1997-12-24
FRICA FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 1
SOFTWARR: Patentin Ver: 2.1
US-09-791-537-32088
US-09-791-537-32088
US-09-794-84-11094
US-09-794-84-11094
US-09-794-84-11094
US-09-794-837-11094
US-09-794-837-110913
US-09-791-537-10913
US-09-791-537-10913
US-09-791-537-94436
US-09-791-537-9496
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US-09-791-537-9085
US-09-791-537-9085
US-09-794-841-9
US-09-794-841-9
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US-09-794-841-5
US-09-798-427-7049
US-09-798-427-5049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHOFIELD, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09582486 GENERAL INFORMATION:
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  1629
1624
1186.5
965.5
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   ; Search time 175 Seconds (without alignments)
1617.056 Million cell updates/sec
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1 MDTTVPTFSLAELQQGLHQD.....ATFQDWIGGNYVNIRRTSKA 311
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                                                                                                                                                                                                                                                                                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence i, Appli

311 19 US-09-582-486-1

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Result No.

Sequence 106840 Sequence 50491, A Sequence 50490, A Sequence 15162, A Sequence 18920, A

Sequence 18920

Sequence 62424,

Sequence 53454 Sequence 72059

Sequence 59894, Sequence 17598, Sequence 136698 Sequence 52863,

Sequence 77409

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PAPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE PARENTIN VERSION 3.0
SEQ ID NO 11094
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PRHHYAAPRRDQIAGSSRISSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                        241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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GENERAL INFORMATION:
APPLICANT: Dilley, David R
APPLICANT: Kadyzhanova, Dina K
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MG141-453
CURRENT APPLICATION NUMBER: US/09/924,841
CURRENT FILING DATE: 200-108-08
PRIOR APPLICATION NUMBER: US/09/413,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.4%; Score 1627; DB 22; Length 311; Best Local Similarity 99.4%; Pred. No. 1.2e-177; Matches 309; Conservative 1; Mismatches 1; Indels 0
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US-09-791-537-11094
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US-09-924-841-18
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US-09-791-537-32088
US-09-791-537-32088
US-09-791-537-32088
Sequence 32088, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: WETHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN version 3.0
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                                                                                         Score 1637; DB 19;
Pred. No. 8.5e-179;
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Pred. No. 7.1e-178;
0; Mismatches 1;
                                                                                                                                        0; Mismatches
; TYPE: PRT
; ORGANISM: Streptomyces clavuligerus
US-09-582-486-1
                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 311; Conservative 0
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Best Local Similarity 99.7%;
Matches 310; Conservative (
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US-09-791-537-32088
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63 AEKKAVMTPIPTIRRGYAGLESESTAQITNTGKYTDYSMSYSMGTADNLFPSAEFEKAWE 122
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                                                                                                     181 APHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 240
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                                                                                                                                                                                                                                                                                                  243 PKHHVAAPGADKRVGSSRTSSVFFLRPNGDFRFSVPRARECGFDVSIPAETATFDDMIGG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Martin, Juan P.
APPLICANT: Coque, Juan R.
APPLICANT: Enguita, Francisco J.
APPLICANT: Puente, Juan L.
APPLICANT: Llarena, Francisco J.
APPLICANT: Liarena, Francisco J.
APPLICANT: Liarena, Paloma
APPLICANT: Liras, Paloma
APPLICANTION: LATE GENES
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/233,605
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GENERAL INFORMATION:
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STREET: P.O. Box 2000
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFRENCE/DOCKET NUMBER: 1917;
TELECOMMUNICATION INFORMATION:
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Matches 186; Conservative
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303 NYINIRKTAAA 313
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CORRESPONDENCE ADDRESS:
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USA
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STRANDEDNESS: si
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified DAOCS
OTHER INFORMATION: from Streptomyces clavuligerus
NAME/KEY: MUTAGEN
LOCATION: (181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.5%; Score 1186.5; DB 22; Length 314; 69.8%; Pred. No. 7.1e-127; ive 41; Mismatches 52; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                         Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                     ; LOCATION: (181)
; OTHER INFORMATION: Ala181 in native DAOCS modified to Arg
US-09-924-841-18
                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.2%; Score 1624; DB 24; Best Local Similarity 99.4%; Pred. No. 2.7e-177; Matches 309; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 121286, Application US/09791537
GENERAL INPORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), ORGANISM: Streptomyces lactamdurans
US-09-791-537-121286
                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
       PRIOR FILING DATE: 1999-10-06
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Best Local Similarity 69.8%,
Matches 217; Conservative
                              NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 311
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US-09-791-537-121286
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TYPE: PRT
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Sequence 10913, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: WETHOOS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
CURRENT FILING DATE: 2001-02-22
SOFTWARE: Patentin version 3.0
SEQ ID NO 10913
LENGTH: 310
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                                                                           62 EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                                                                                                                                    122 YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMA 181
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DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA 61
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59.0%; Score 965.5; DB 22; Length
Best Local Similarity 61.2%; Pred. No. 2e-101;
Matches 186; Conservative 37; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Streptomyces lactamdurans
US-09-791-537-10913
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   EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                       62 BKQAVTTKVPIMRRGYSALEAESTAQVTNTGTYTDYSMSYSMGIGGNLFPSKEFESVWTD 121
                                                                             YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMA 181
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GENERAL INFORMATION:
APPLICANT: Martin. Juan F.
APPLICANT: Enguita, Francisco J.
APPLICANT: Fuence, Juan L.
APPLICANT: Pleare, Francisco J.
APPLICANT: Liras, Paloma
TITLE OF INVENTION: LATE GENES
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.0%; Score 965.5; DB 11; Length Best Local Similarity 61.2%; Pred. No. 2e-101; Matches 186; Conservative 37; Mismatches 80; Indels
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MEDIUM TYPE: FIDOPDY disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,468
FILING DATE: 22-OCT-1996
CLASSIFICATION NUMBER: 08/23,605
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REPERENCE/DOCKET NUMBER: 35,403
TELECOMMUNICATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: John W. Wallen III STREET: P.O. Box 2000 CITY: Rahway STATE: New Jersey STATE: New Jersey STATE: New Jersey STONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 310 amino.
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-727-468-6
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Sequence 94436, Application US/09791537

Sequence 94436, Application US/09791537

GRNERAL INFORMATION:
APPLICANT: Bonomix, Inc.
APPLICANT: Bonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: MATHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PELLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 94416
LENGTH: 332
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                                                                        62 EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
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                  122 YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMA
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                                                                                                                                                                                                                                                                                                                   242 RHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGGN
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Best Local Similarity 56.7°
Matches 177; Conservative
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301 GNYVNMRRDKPA 312
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US-09-791-537-94436
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                                                                    APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Inc.
APPLICANT: Bobo, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 10914
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFDRQYTASRAVAREVLRATG---TEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMAPHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLYTGGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                             57.4%; Score 939.5; DB 22; Length 318; 58.6%; Pred. No. 2.1e-98; ive 43; Mismatches 81; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.2%; Score 937; DB 22;
58.0%; Pred. No. 4.1e-98;
iive 45; Mismatches 83;
                                   Sequence 10914, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Lysobacter lactamgenus US-09-791-537-4795
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 58.6
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.2
Best Local Similarity 58.0
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGNYVNI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 GTNYVTM 309
RESULT 9
US-09-791-537-10914
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US-09-791-537-4795
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                                                                                                                                                                                                                                                                                                LENGTH: 318
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DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
11;
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                                                                                                                                                                                                                                                                                                         126 VNLWPDEEKHPRFRPFCEDYYRQLLRLSTVIMRGYALALGRREDPFDEALAEADTLSSVS 185
                                                                                                                                                                                                                                                                                                                                                                                                             186 LIRYPYLEEYPPVKTGADGTKLSFEDHLDVSMITVLYQTEVQN----LQVETVDGWQDIP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 TDEEKYDLAINAYNKNNPRTRNGY-----YMAVKGKKAVESWCYLNPSFSEDHPQI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 -SG---DFGRIW------TQYFDRQYTASRAVAREVLRATGTEPDGGVEA--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 ---FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GSEAEK-----RAVISPVPIMRRGF----IGLESESTAQIINIGSYSDYSMCYSMGTAD- 107
                                                                               10 VPIDISPLSGDDAKAKQRVAQ-EINKAARGSGFFYASNHGV---DVQLLQDVVNEFHRN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 TADGWQDLPTSGENFLVNCGTYMGYLTNDYFPAPNHRV-----KFINAERLSLPFFL 284
                                                                                                                                                                                                                                                                                                                                                           LLRFRYFPQVPEHRS-AEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VPTFSLAELQOGLHQD-----EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 VPIIDISPLSGGDADDKKRVAQEINKACRESGFFYASHHGI----DVQLLKDVVNEFHRTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 SEAEK-----RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFP--
                                                  ---AELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
Gaps
                                                                                                                                                                                                                                                         108 -NLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCE--
42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 YRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 RSDEDFLVNCGTYMGHITHDYFPAPNHRV-----KFINAERLSLPFFL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 329;
45; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 176; DB 22; 24.5%; Pred. No. 2.2e-10; iive 39; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9085, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Balonomix, Inc.
APPLICANT: Debc, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCT'
TITLE OF INVENTION: MITHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNDBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SERVICH: 329
LENGTH: 329
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; Sequence 12239, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Streptomyces griseus
US-09-791-537-9085
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 24.5
Matches 73; Conservative
                                                  5 VPTFSL---
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US-09-791-537-9085
                                                                                                                                                                                                                                                                                                                                                              158
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                                                                                                                                                                                                 APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPREBLOCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 89857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 IKAPQHRVVSPGAAQRIGSNRTSSVLFLRPKSERSFSVPLAKALGMGDDLVGERATFGEW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 NRMAPHYDLSIVSLILGTPCPNGFVSLQVEIDGRFVEVPPRPGCVVVFCGSIAPLVSDGK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 ADDAAKQAVINANPNTRRGFSPLGSESTARCTNTGDYSDYAMVYSMGISGNIFPTAHFER 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 313;
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Pred. No. 9.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 852; DB 22;
52.9%; Pred. No. 2.5e-88;
iive 48; Mismatches 91;
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8-09-791-537-89857
; Sequence 89857, Application US/09791537
; GENERAL INFORMATION:
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; ORGANISM: Streptomyces jumonjinensis
US-09-791-537-89857
                                                                                                    Sequence 4796, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Lysobacter lactamgenus
US-09-791-537-4796
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Best Local Similarity 52.9
Matches 165; Conservative
                                                                                                                                                    APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
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Best Local Similarity
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APPLICANT: States, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12239
LENGTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 SWYDVDPIPGTLVVNIGELLELASNGYLRATVHRVVTPP----AGVERISVPFFFSARLD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 EHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 AL-PEADKLAIEMVKSSQFRGYTRAGGELTK-----GREDWREQLDIGVERQAIAQGPG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 GRIWTQ-YFDRQYTAS------RAVAREVLRATGTEPDGGVEAFLDCEPLL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TPAWTRLQGPNQWPAALPDLKPALLAWQSKVTAVAIRLLKAFAQSLDQPEDAF---DPI- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 RFRYFPQVPEHR-SAEEQPLR------MAPHYDLSMVTLIQQTPCANGFVSLQAEVGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AFTDLPYRPDAVLVFCGALATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 MPRIVPVLDLSRLEQGASERRIFLADLRSASRDIGFFYLAGHGISWAEISEVLTASRQFF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDTTVPTFSLAELQQGLHQ-----DEPRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.3%; Score 168; DB 29; Length 366; Best Local Similarity 24.7%; Pred. No. 2.1e-09; Matches 85; Conservative 41; Mismatches 158; Indels 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 ATIPLLGLSEELAAQARGPAS-DPDNPLFRD-VGTNVLKSRLRS 346
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Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Mesorhizobium loti
US-10-369-493-12239
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US-10-679-063-16144
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63175, A
62424, A
53454, A
72059, A
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36, Appl
16, Appl
7737, Ap
66945, A
3232, Ap
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9242, Ap
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Sequence 16144, A
Sequence 22244, A
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                                                                                     (without alignments)
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'cgn2_6/ptodata/2/paa/VGS0_NEW_COMB.pep:*

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'cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

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(c) 1993 - 2004 Compugen Ltd.
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US-10-679-063-16144

US-10-425-114A-58433

US-10-425-114A-63175

US-10-425-114A-63175

US-10-425-114A-63175

US-10-425-114A-63135

US-10-425-114A-72059

US-10-679-063-13321

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US-10-679-063-9242

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US-10-679-063-9242

US-10-679-063-9242

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US-10-739-930-6723
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US-10-679-063-15920
US-10-679-063-9241
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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No.
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w	sednence 170, App	Sequence 26257, A	Sequence 11, Appl	Sequence 26262, A	Sequence 14, Appl	Sequence 21222, A	Sequence 23016, A	Sequence 14972, A	Sequence 7978, Ap	Sequence 26255, A	Sequence 49881, A	Sequence 8, Appli	Sequence 11737, A	Sequence 24496, A	Seguence 125, App	Sequence 26256, A	Sequence 124, App	Sequence 17, Appl
Sedu	Sedn	Sedn	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedn	Sedu
US-10-425-114A-61225	US-10-715-872-126	US-10-679-063-26257	US-10-257-494A-11	US-10-679-063-26262	US-10-257-494A-14	US-10-679-063-21222	US-10-679-063-23016	US-10-679-063-14972	US-10-679-063-7978	US-10-679-063-26255	US-10-425-114A-49881	US-10-257-494A-8	US-10-679-063-11737	US-10-679-063-24496	US-10-715-872-125	US-10-679-063-26256	US-10-715-872-124	US-10-257-494A-17
356 6	356 6	382 6	382 6	370 6	370 6	335 6	337 6	389 6	392 6	339 6	371 6	386 6	371 6	339 6	356 6	371 6	355 6	377 6
7.7	7.7	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.5	7.5					7.4	7.4	7.4
126.5	126	125	125	124.5	124.5	124	124	124	124	123	123	122.5	122	121	121	121	120.5	120.5
27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120 216 PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV 275 234 PPRPGTFAVNIGELLELATNGYLKATVHRVVSPPAD----SDRLSIAFFL--GARLGSKV 287 72 DEKRAIDMVNSPHFHGYTRVGAELTR-----GAPDWREQLDIGSERPLLPQGPDTPAWA 125 126 RIQGPNQWPAALPDLRAAVIRLQAELTAVALALLERIALAIGERAD----FFADLYEGGP 181 156 EPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 6 PTFSL-ABLOOGLHODEF----RRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFPEHGSE APPLICANT: Edgerton, Michael D
TITLE OF INVESTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
FILE REFERENCE: 38-15(52054)B
CURRENT PAPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 16188
LENGTH: 345 Length 345; 10.7%; Score 174.5; DB 6; 26.8%; Pred. No. 8e-09; iive 32; Mismatches 134; US-10-679-063-16188 ; Sequence 16188, Application US/10679063 ; GENERAL INFORMATION: ORGANISM: Rhodospirillum rubrum Best Local Similarity 26.84 Matches 81; Conservative

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76 LNSP---OFRGYTRTGTEYTAGSAYWREQIDIGPEREALALGPDDPDYLRLIGPNQWPSA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.5%; Score 155; DB 6; Best Local Similarity 23.4%; Pred. No. 6.7e-07; Matches 78; Conservative 49; Mismatches 119,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 PIMPTTDCLIG-PAREFLSDDNPPCYRTLTPADF 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 FLRPNADFTFSVPLARECGFDVSLDGETATFQDW 297
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US-10-425-114A-63175
Sequence 63175, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 VFAAALGQAEDVFEPIYVPSPNQLIKIIRYPGRAADESDQGVGTHKDSGFVTILLQDTVA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPE----- 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 LPVLDLSRFRSDTAERAĒFLRDVRDAAFGPĞFFYLVGHĞISDRLIRDVLFASRNFFAL-P 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAEK---RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 EADKLDIEMINSP---HFRGYTRAGREFTR-----GQPDWREQLDVGAEREAFPLSRSA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 NGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHVAAPRRDQIAGSSR 258
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|LAELRSAAH-----EVGFFYVTGHGVPAPLRDEVLSAARAFFALPVERRLEIEN- 75
                                                                                                                                                                                                                                                                                                                                                                                                                       5 VPTPSLAELQQG-LHQDEPRRCLRD----KGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 TSSVFFLRPNADFTFSV----PLARECGFDVSLDGETATFQDWIGGNYVNIRRTS 309
                            APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)8
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 16144
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TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT PILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 22244
                                                                                                                                                                                                                                                                                                                                     10.3%; Score 169; DB 6; Length 412;
.larity 23.9%; Pred. No. 3.4e-08;
Conservative 39; Mismatches 141; Indels
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28.1%; Pred. No. 2e-07;
ive 33; Mismatches 118; Indels
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US-10-679-063-22244
Sequence 16144, Application US/10679063 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22244, Application US/10679063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           ORGANISM: Rhodopseudomonas palustris
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Matches 85; Conserv
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Best Local
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...ru, Jingdong
...rulcanr: Kovalic, David K.
...rulcanr: Screen, Steven E
...rulcanr: Screen, Steven E
...rulcanr: Screen, Jack B
...rulcanr: Nucleic Acid Molecules and Other Molecules Associated With
...rulcanrow Nucleic Acid Molecules and Uses Thereof for Plant Improvement
...rulcanrow Numbers US/10/425,114A
...rulcanrow Numbers US/10/425,114A
...rulcanrow Numbers OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 PAEDKA------GLYSEDTGRATRIYSSTMFDTGAEKYWRDCLRLACS---FP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 S-GDFGRIW------TQYFDRQYTASRAVAREVLR----ATGTEPD------GGVEAF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 LDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAF 212
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                                             186 YPP--RAAEDADOGVGAHKDYGYLALLLQQDEV--GGLQVQREDGEWIDAVPV-PDAFVFN 240
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114 -----DFGRIWTQYFDRQYTASRAVAREVLRATGT---EPDGGVEAFLDCEPLLRFRYFP
                                                                                                                                           166 QVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVF
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                                                                                                                                                                                                                                                                                                                                        241 IGEMLEIATQGYLKATQHRVVSPQ----AGVHRYSIPFFLGPRLD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                              226 CGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: LIB3587-225-H12_FLI.pep
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APPLICANT: Lu, Jingdong
Labou, Yhuua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: APPLICANT: Abaska, Jack E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5:3454
LENGTH: 372
TYPF. TYPF.
                                                                                                                                                                                                                                                                                                                      60 BAEKRAVTSPVPTWRRGFTGLESESTAQIT------NTGSYSDYSMCYSMGTADNLFP 111
                                                                                                                                                                                                                                                                                      112 S-GDFGRIW------TQYFDRQYTASRAVAREVLR----ATGTEPD------GGVEAF 152
                                                                                                                                                                                                                                                                                                                                                                                           153 LDCEPLLRFRYFPQVPEHRSABEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                           218 ---DVVLHVNHYPPCPDPNAT----LGLPPHCDRNLLTLL------LPSMVPG-- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 TOLPYR-----PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 LEVAYRGDWIRVEPVPGAFVVNFGCQLEVVTNGILKSIEHRVMTN-----LGVARTTVAT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 EAEKRAVTSPVPTMRRGFTGLESESTAQIT-----NTGSYSDYSMCYSMGTADNLFP 111
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                                                                             4 TVPTFSLAELQQGLHQDEFRRCL----RDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
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Best Local Similarity 23.4%; Pred. No. 1e-06;
Matches 78; Conservative 48; Mismatches 120; Indels 88; Gaps
                             88;
                             Indels
     ; Pred. No. 1e-06;
48; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 FIMPTIDCLIG-PARELSDDNPPCYRTLTFGDF 345
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US-10-425-114A-53454
     23.4%;
                          78; Conservative
Best Local Similarity
Matches 78; Conserv
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APPLICANT: Screen, Screen B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Danies and Uses Thereof for Plant Improvement TITLE REFERENCE: 38-21(53113)B
CURRENT PAPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                     APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5331) B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 63175
LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 TOLPYR-----PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 154; DB 6; Length 352; Best Local Similarity 23.4%; Pred. No. 7.7e-07; Matches 78; Conservative 49; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: LIB3062-030-F8_FLI.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 FLRPNADFTFSVPLARECGFDVSLDGETATFQDW 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 62424, Application US/10425114A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.3%;
                          Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-114A-63175
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                                                                             APPLICANT:
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| Sequence 4, Application US/10481381
| Sequence 4, Application US/10481381
| Sequence 4, Application Sequence 5, Sequence 6, Applicant Okawa, Miho
| APPLICANT: Okawa, Miho
| APPLICANT: Matsuoka, Makoto
| APPLICANT: Applikari, Motoyuki
| TITLE OF INVENTION: 8d1 gene involved in plant semidwarfing and uses thereof
| TITLE OF INVENTION: 8d2 gene involved in plant semidwarfing and uses thereof
| CURRENT APPLICATION NUMBER: US/10/481,381
| CURRENT APPLICATION NUMBER: US/10/481,381
| PRIOR FILING DATE: 2003-12-18
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 4
| LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                  145 FSFKLPWKETLSFRSSAQPDSSNIVQDY-LCNTMG--EDFKP---FGKVYQDYCDAMSTL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 SLGIMELLGWSLGVSQGHYREFFEENESIMRLNYYPPCQKP-----DLTLGTGPHCDPT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 QITNIGSYSDYSMCYSMGTAD----NLFPSGDF---GRIWIQYFDROYTASRAVAREVLR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 ATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCAN 199
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                                                                                                                                                                                                                                                                                    92 GFFLVVNHGVDDKLIAHAHQYIDYFFELPMSAKQRA-----QRKVGEHCGYASSFTGR 144
                                                                                                                                                                                                                                                                                                                                                      80 ------LESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFF--QVPEHRSAEEQFLRMAPHYDLS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 SLIILHQD------QVGGLQVFVDEEWRSITPNFNAFVVNIGDTFWALSNGRYKS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 MYTLIQQTPCANGFVSLQAEVGG--AFTDLPYRP-----DAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRRGFTGLESE---STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GFVSLQAEVGG--AFTDLPYR-----PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 389;
                                                                                                                                                       Length 379;
                                                                                                                                                    9.3%; Score 152; DB 6; Length 37 24.3%; Pred. No. 1.3e-06; tive 40; Mismatches 105; Indels
                                                                                                                                                                                                                                                        30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVP 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 CLHRAVVNSK-----TPRKSLAFFLCPKNDKVVSPP 332
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                                                                                                                                                                            Best Local Similarity 24.3%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 24.8
Matches 64; Conservative
                          ; LENGTH: 379
; TYBE: PRT
; ORGANISM: Fagus sylvatica
US-10-679-063-13321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
  SEQ ID NO 13321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-481-381-4
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihuan APPLICANT: Zhou, Yihuan APPLICANT: Zhou, Yihuan APPLICANT: Screen, Steven E APPLICANT: Screen, Steven E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: 19111531318 CURRENT APPLICATION NUMBER: 105/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DVVLHVNHYPPCPDPNAT----LGLPPHCDRNLLTLL------LPSMVPG-- 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AVGDSAAAWPDKPRRLREVVERFTVQTRGLGMBILRLLCEGLGLRPDYLEGDISGG---- 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 TDLPYR-----PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TVPTFSLAELQQGLHQDEFRRCL----RDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
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GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15/52064)B
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
NUMBER OF SEQ ID NOS: 27373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
9.3%; Score 153; DB 6; Length 372;
Best Local Similarity 23.4%; Pred. No. 1e-06;
Matches 78; Conservative 48; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: LIB3245-358-A7_FLI.pep
US-10-425-114A-72059
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                                                                                                                             314 FIMPTTDCLIG-PAAEFLSDDNPPCYRTLTFGDF 346
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                                                                                                                                                                                                                                                     ; Sequence 72059, Application US/10425114A; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
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US-10-425-114A-72059
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US-10-679-063-13321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --OYFDRQYTASRAVAREVLR------ATGTEPDGGV--EAF--LDCEPLLRF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 NYYPPCPR----PDLALGVVAHTDLSALTVL----VPNEVPGLQVFKDDRWIDAKYIPNA 255
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GENERAL INFORMATION:
BAPLICANT: BASE PLANT SCIENCE GMBH
TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS IV
FILE REFERENCE: 16313-0236
CURRENT APPLICATION NUMBER: PCT/US03/24364
CURRENT PILING DATE: 2003-08-04
PRIOR PLING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENT VERSION 3.2
SOFTWARE: PATENT VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 335;
                                                                                                                                        APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
NUMBER OF SEQ ID NOS: 27373
SEO ID NO 9242
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                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 137.5; DB 6; Length 21.8%; Pred. No. 2.8e-05; tive 47; Mismatches 124; Indels
                                                                         RESULT 11
Sequence 9242, Application US/10679063
GENERAL INFORMATION:
LENGTH: 380
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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Best Local Similarity 21.8<sup>†</sup>
Matches 63†, Conservative
                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Citrus unshiu US-10-679-063-9242
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Les 69; Conserva
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PCT-US03-24364-36
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APPLICANT: AN, GYN-HEUNG
APPLICANT: ANG, HOUG-GOU
APPLICANT: ANG, KI-HWAN
APPLICANT: DARK, YONG-JOO
APPLICANT: DARK, YONG-JOO
APPLICANT: DARK, YONG-JOO
APPLICANT: DARK, YONG-JOO
APPLICANT: DEE, SANG-YEB
TITLE OF INVENTION: A PROMOTER CV200xP WHICH REGULATES THE INTECUMENT-SPECIFIC
TITLE OF INVENTION: SEEDS OF WATERMELON AND A METHOD FOR GENERATING SEEDLESS
TITLE OF INVENTION: FRUITS USING THE PROMOTER
FILE REFERENCE: 7022-0003
TITLE OF INVENTION: FRUITS USING THE PROMOTER
FILE REFERENCE: 7022-0003
CURRENT APPLICATION NUMBER: US/10/257,494A
CURRENT APPLICATION NUMBER: PCT/KR00/01127
PRIOR APPLICATION NUMBER: RX 2000/18483
PRIOR FILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: X 2000/18483
PRIOR FILING DATE: 2000-04-08
NUMBER OF SEQ ID NOS: 18
SSOF ID NO 16
LENGTH: 380
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                                                                                                                                                                                                                                                                                                                                               229 NYYPQCKQ----PELALGTGPHCDPTSLTILHQDQVG----GLQVFVDNKWQSIPPNPHA 280
                                                                                                                                               161
                                                                                                                                                                                           170 -FVSKKMCDGYEDFGKVYQEYARAMNTLSLKIMELLGMSLGVERRYFKEFFEDSDSIFRL 228
                                                                                                                                                                                                                                                                                                   221
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GFTG-LESESTAQITNTGSYSDYSMCYSMGTADN 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 PACEKQ-----KAQRKWGESSGYASSFVGRFSSKLPWKETLSFKFSPEEKIHSQTVKD-
                                                                   117 PACEKO-----KAQRKWGESSGYASSFVGRFSSKLPWKETLSFKFSPEEKIHSQTVKD-
                                                                                                                                               109 LPPS-----GDFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRF
                                                                                                                                                                                                                                                                                                   162 RYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 VLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVP 276
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8.3%; Score 136.5; DB 6;
Best Local Similarity 23.4%; Pred. No. 4.1e-05;
Matches 69; Conservative 38; Mismatches 143;
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ORGANISM: Arabidopsis thaliana
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Screen, Screen, Screen, Steven E
APPLICANT: Screen, Sc
Sequence 7737, Application US/10739930
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION:
US. 138-21 (153377)
CURRENT FILING DATE: 2003-12-18
SEQ ID NO 7737
LENGTH: 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --QIŢNTGSYSDYS-----MCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVLR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 SLGVELRGYYREFFEDSRSIMRCNYYPPCPE----PERTLGTGPHCDPTALTILLQDXDV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 135.5; DB 6; Length 405; 24.2%; Pred. No. 5.5e-05; Live 41; Mismatches 123; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C24992_1.p
US-10-739-930-7737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: LIB4756-039-A6_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(405)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 66945, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.2'
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 TSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 RSLAFFLCPRED 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-425-114A-66945
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DB 6; Length 385;

Score 133;

8.18;

Query Match

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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 PDLVMGLSAHSDGSAVTVLQQDV---GCAGLQVRGKGGAWVPVHPVFHALVVNIGDTLEV 289
                                                                                                                                                                                                                                                                                                                                                                   62 EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGT-----ADNLFPS--G 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::: :| |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 DFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 EEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE-VGGAFTDLPYRPDAVLVFCGAIATL 232
                                                                                                                                                                                                                                            5 VPTFSLAELQQ---GLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA 61
                                                                                             34; Gaps
        1 Similarity 21.9%; Pred. No. 9e-05; 61; Conservative 43; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 VTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
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Matches 61; Conserva
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